GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p_model

Run on: March 21, 2006, 19:33:19 ; Search time 20.8621 Seconds
(without alignments)
1529.038 Million cell updates/sec

Title: US-10-679-032-27
Perfect score: 670
Sequence: 1 gaggtgcagctgttggagtc.....cactggtcaccgtgagctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122106_13617/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_476_@runat_21032006_122106_13617 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	535	79.9	123	9	ADZ41228	Adz41228 Anti-HAS
2	528.5	78.9	120	8	ADL92395	Adl92395 Single do
3	528.5	78.9	120	8	ADQ77003	Adq77003 TAR2-10 p
4	527	78.7	224	7	ADJ32114	Adj32114 Human int
5	522.5	78.0	116	6	ABP95999	Abp95999 HSA antib
6	522.5	78.0	116	8	ADL92382	Adl92382 Anti-HSA
7	522.5	78.0	116	8	ADQ14599	Adq14599 Single-do
8	522.5	78.0	116	8	ADQ77187	Adq77187 Dummy VH
9	522.5	78.0	116	8	ADQ77171	Adq77171 VH dummy
10	522.5	78.0	116	8	ADQ90914	Adq90914 Vh chain
11	522.5	78.0	116	8	ADS78329	Ads78329 DP47-JH4b
12	522.5	78.0	116	8	ADT88238	Adt88238 Human ant
13	522.5	78.0	116	8	ADU86514	Adu86514 Immunoglo
14	522.5	78.0	116	9	ADZ41141	Adz41141 Dummy VH
15	522.5	78.0	240	2	AAY02472	Aay02472 A single
16	522.5	78.0	240	6	ABP95997	Abp95997 Human ser
17	522.5	78.0	240	8	ADL92369	Adl92369 Human pha
18	522.5	78.0	240	8	ADQ77165	Adq77165 HSA Heavy
19	521	77.8	119	2	AAR23739	Aar23739 Recombina
20	521	77.8	119	2	AAR41721	Aar41721 Aglycosyl
21	521	77.8	119	6	ABP98804	Abp98804 Chimeric
22	521	77.8	119	7	ADH59067	Adh59067 CDR antib
23	521	77.8	131	9	ADW04866	Adw04866 PAPP-A im
24	521	77.8	131	9	ADW04842	Adw04842 PAPP-A im
25	521	77.8	147	9	ADY33975	Ady33975 Anti-Tie
26	521	77.8	449	3	AAY68810	Aay68810 A rat hea
27	520	77.6	125	9	ADV14356	Adv14356 Hybridoma
28	520	77.6	131	9	ADY34015	Ady34015 Anti-Tie
29	520	77.6	136	9	ADY70946	Ady70946 Human mon
30	520	77.6	276	8	ADO25149	Ado25149 Melanoma
31	520	77.6	455	9	ADY70958	Ady70958 Human mon
32	520	77.6	474	5	AAO14065	Aao14065 Heavy cha
33	520	77.6	474	6	ABU08017	Abu08017 Human mon
34	520	77.6	474	7	ADF65775	Adf65775 Human mon
35	520	77.6	474	8	ADJ92515	Adj92515 Human SOJ
36	518	77.3	227	4	AAB75051	Aab75051 TRO005 Hu
37	518	77.3	250	8	ADS09246	Ads09246 Human c-M
38	516	77.0	123	6	ABR55827	Abr55827 Heavy cha
39	516	77.0	138	5	ABG76932	Abg76932 Humanised
40	516	77.0	138	8	ADR88416	Adr88416 Humanised
41	516	77.0	248	8	ADI58087	Adi58087 Reg IV-sp
42	515.5	76.9	132	9	ADW04762	Adw04762 PAPP-A im
43	515.5	76.9	253	8	ADI58060	Adi58060 Reg IV-sp
44	515	76.9	451	8	ADH34584	Adh34584 008 heavy
45	514.5	76.8	116	8	ADQ90916	Adq90916 Vh chain

ALIGNMENTS

RESULT 1
ADZ41228
ID ADZ41228 standard; protein; 123 AA.
XX
AC ADZ41228;
XX
DT 30-JUN-2005 (first entry)
XX
DE Anti-HAS domain antibody TAR3h-22.
XX
KW Single chain antibody; antibody engineering; inflammation;
KW antiinflammatory; sepsis; antibacterial; immunosuppressive; infection;
KW hypersensitivity; antiallergic; immunosuppressive; immune disorder;
KW cancer; cytostatic; neoplasm; autoimmune disease; diabetes; antidiabetic;
KW endocrine disease; gastrointestinal disease; metabolic disorder;
KW rheumatoid arthritis; antiarthritic; antirheumatic;
KW musculoskeletal disease; multiple sclerosis; neuroprotective;
KW neurological disease; Crohns disease; gastrointestinal-gen.;
KW gastrointestinal disease; ulcerative colitis; antiulcer; aplastic anemia;
KW antianemic; hematological disease; hashimotos disease; antithyroid;
KW graves disease; reiter's syndrome; ophthalmological; uropathic;
KW transplant rejection; graft versus host disease; pulmonary disease;
KW respiratory-gen.; respiratory disease; pulmonary fibrosis;
KW myocardial ischemia; cardiant; vasotropic; cardiovascular disease;
KW bone disease; osteopathic; hepatitis; hepatotropic; reperfusion injury;
KW injury; fever; antipyretic; temperature disorder.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2005035572-A2.
XX
PD 21-APR-2005.

```
XX
PF   08-OCT-2004; 2004WO-GB004253.
XX
PR   08-OCT-2003; 2003US-0509613P.
PR   08-JAN-2004; 2004US-0535076P.
PR   30-JUN-2004; 2004WO-GB002829.
XX
PA   (DOMA-) DOMANTIS LTD.
XX
PI   Tomlinson I,  Basran A,  Jones P;
XX
DR   WPI; 2005-306343/31.
XX
PT   Composition useful for treating or preventing sepsis, autoimmune
PT   disorders and pulmonary disorders, comprises polypeptide having single
PT   human immunoglobulin variable domain that binds polypeptide antigen, e.g.
PT   human cytokine.
XX
PS   Example 11; SEQ ID NO 89; 169pp; English.
XX
CC   The invention relates to a composition comprising a polypeptide having a
CC   single human immunoglobulin variable domain that binds a polypeptide
CC   antigen with Kd less than or equal to 100 nM, where the polypeptide is
CC   present at a concentration of at least 400 microM as determined by
CC   absorbance of light at 280 nm wavelength. The polypeptides are termed
CC   domain antibodies (dAb) and may occur as homodimers or heterodimers
CC   (where the second polypeptide is a partner dAb which does not bind to the
CC   target protein_ linked via (Gly4Ser)n linkers. The adAb polypeptides
CC   contain human framework regions, synthetic/modified complementarity
CC   domains (CDR) or contain mutations at positions defined in the
CC   specification. dAb antibodies were created which bind to TNFalpha, TNF
CC   receptor (p55), mouse serum albumin (MSA) and human serum albumin (HSA).
CC   The polypeptide is useful for treating or preventing a disease or
CC   disorder in an individual in need of treatment, which involves
CC   administering the polypeptide to the individual. The polypeptide (or an
CC   extended release dosage formulation containing it) is useful for
CC   preventing or treating diseases or disorders related to target antigens,
CC   such as inflammation, sepsis, allergic hypersensitivity, cancer,
CC   autoimmune disorders (e.g., diabetes, rheumatoid arthritis, multiple
CC   sclerosis, Crohn's disease, ulcerative colitis, aplastic anemia,
CC   Hashimoto's disease, Graves disease, Reiter's syndrome), transplant
CC   rejection, graft versus host disease, pulmonary disorder (e.g., pulmonary
CC   fibrosis, pulmonary sarcoidosis), cardiac disorders (e.g., ischemia of
CC   heart), inflammatory bone disorders, hepatitis, reperfusion injury and
CC   pyrexia. The polypeptide comprises single immunoglobulin variable domain
CC   polypeptides that bind target antigen with high affinity and are soluble
CC   at high concentration, without aggregation or precipitation. The present
CC   sequence represents a dAb antibody of the invention.
XX
SQ   Sequence 123 AA;

Alignment Scores:
Pred. No.:              7.02e-42        Length:         123
Score:                  535.00          Matches:        106
Percent Similarity:     87.0%           Conservative:   1
Best Local Similarity:  86.2%           Mismatches:     14
Query Match:            79.9%           Indels:         2
DB:                     9               Gaps:           1

US-10-679-032-27 (1-363) x ADZ41228 (1-123)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheSerLysTyrTrpMetSerTrpValArgGlnAla 40

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerSerIleAspPheMetGlyProHisThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::   |||
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysGlyArg 100

Qy        301 GTGGGT------CCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACC 354
                  |||      |||   ||||||||||||||||||||||||||||||||||||||
Db        101 ThrSerMetLeuProMetLysGlyLysPheAspTyrTrpGlyGlnGlyThrLeuValThr 120

Qy        355 GTGAGCTCA 363
              |||||||||
Db        121 ValSerSer 123

RESULT 2
ADL92395
ID   ADL92395 standard; protein; 120 AA.
XX
AC   ADL92395;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Single domain antibody (dAb)-related TAR2-10 protein.
XX
KW   immunoglobulin single variable domain; cytostatic; antiinflammatory;
KW   antirheumatic; antiarthritic; antiasthmatic; antiallergic; antibacterial;
KW   virucide; immunosuppressive; antidiabetic; neuroprotective; muscular;
KW   dermatological; gene therapy; inflammatory; rheumatoid arthritis; asthma;
KW   Crohn's disease; allergic hypersensitivity; bacterial; viral infection;
KW   autoimmune disorder; type I diabetes; multiple sclerosis;
KW   myasthenia gravis; systemic lupus erythematosus; cancer;
KW   single domain antibody; dAb; TAR2-10.
XX
OS   Unidentified.
XX
PN   WO2004003019-A2.
XX
PD   08-JAN-2004.
XX
PF   30-JUN-2003; 2003WO-GB002804.
XX
PR   28-JUN-2002; 2002WO-GB003014.
PR   27-DEC-2002; 2002GB-00030202.
XX
PA   (DOMA-) DOMANTIS LTD.
XX
PI   Winter G,  Tomlinson I,  Ignatovich O,  Holt L,  De Angelis E;
XX
DR   WPI; 2004-142855/14.
DR   N-PSDB; ADL92396.
XX
PT   New dual-specific ligands, useful in drug discovery and development, or
PT   for diagnosing, preventing or treating a disease, such as cancer,
PT   autoimmune disease, or inflammatory disease, including rheumatoid
PT   arthritis or asthma.
XX
PS   Disclosure; Page 163; 174pp; English.
XX
CC   The invention relates to a novel dual-specific ligand comprising a first
CC   immunoglobulin single variable domain having a binding specificity to a
CC   first epitope or antigen and a second complementary immunoglobulin single
CC   variable domain having a binding activity to a second epitope or antigen.
CC   The ligand of the invention demonstrates cytostatic, antiinflammatory,
CC   antirheumatic, antiarthritic, antiasthmatic, antiallergic, antibacterial,
CC   virucide, immunosuppressive, antidiabetic, neuroprotective, muscular and
CC   dermatological activities and may be useful in gene therapy, ligand
CC   binding assays or for diagnosing, preventing or treating a disease
CC   selected from an inflammatory disease such as rheumatoid arthritis,
CC   asthma or Crohn's disease, an allergic hypersensitivity, a bacterial or
CC   viral infection, an autoimmune disorder such as type I diabetes, multiple
CC   sclerosis, myasthenia gravis or systemic lupus erythematosus or cancer.
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:40:45 ; Search time 4.43319 Seconds
(without alignments)
1575.691 Million cell updates/sec

Title: US-10-679-032-27
Perfect score: 670
Sequence: 1 gaggtgcagctgttggagtc.....cactggtcaccgtgagctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122109_13665/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_77_@runat_21032006_122109_13665 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	515	76.9	119	2	S31108	Ig heavy chain - h
2	514	76.7	140	2	S31686	Ig heavy chain V r
3	512	76.4	119	2	C36005	Ig heavy chain V r
4	509.5	76.0	120	2	S48798	Ig heavy chain V r
5	509.5	76.0	124	2	S20782	Ig heavy chain V r
6	505	75.4	119	2	S31107	Ig heavy chain - h
7	504	75.2	138	2	S31666	Ig heavy chain V r
8	502	74.9	121	2	I55673	Ig heavy chain - h
9	501	74.8	123	2	S31114	Ig heavy chain - h
10	501	74.8	140	2	S31588	Ig heavy chain V r
11	500	74.6	134	2	S31699	Ig heavy chain V r
12	498.5	74.4	136	2	S31587	Ig heavy chain V r
13	498	74.3	117	2	S78486	Ig heavy chain V r
14	497	74.2	139	2	I37781	Ig variable region
15	493	73.6	119	2	D36005	Ig heavy chain V r
16	492.5	73.5	114	2	S31120	Ig heavy chain - h
17	492	73.4	125	2	S30531	Ig heavy chain V r
18	491.5	73.4	116	2	S31110	Ig heavy chain - h
19	490.5	73.2	128	2	S26790	Ig heavy chain V r
20	490	73.1	127	2	S38489	Ig heavy chain - h
21	490	73.1	143	2	S23624	Ig heavy chain V r
22	489.5	73.1	140	2	S70442	Ig heavy chain pre
23	489.5	73.1	147	2	I37780	Ig variable region
24	488	72.8	121	2	S19666	Ig heavy chain V r
25	488	72.8	121	2	G36005	Ig heavy chain V r
26	485	72.4	135	2	S31598	Ig heavy chain V r
27	485	72.4	160	2	S05271	Ig heavy chain pre
28	484	72.2	123	2	S31509	Ig heavy chain - h
29	482.5	72.0	122	2	S31675	Ig heavy chain V r
30	482	71.9	121	2	S26798	Ig heavy chain V r
31	481.5	71.9	118	2	S31105	Ig heavy chain (su
32	481	71.8	140	2	A30532	Ig heavy chain pre
33	480	71.6	119	2	F36005	Ig heavy chain V r
34	479.5	71.6	141	2	S31669	Ig heavy chain V r
35	478.5	71.4	122	2	S31117	Ig heavy chain - h
36	476	71.0	134	2	S31679	Ig heavy chain V r
37	474.5	70.8	135	2	I37778	Ig variable region
38	474.5	70.8	151	2	A60943	Ig heavy chain pre
39	474	70.7	109	2	PH1649	Ig heavy chain V r
40	473.5	70.7	114	2	S46390	Ig heavy chain V r
41	473.5	70.7	118	2	S31116	Ig heavy chain - h
42	473	70.6	121	2	H36005	Ig heavy chain V r
43	472.5	70.5	120	2	S44111	Ig heavy chain V-D
44	472.5	70.5	133	2	S31510	Ig heavy chain - h
45	471	70.3	140	2	S22657	Ig heavy chain pre

ALIGNMENTS

RESULT 1
S31108
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31108
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurma
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31108
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: UNIPARC:UPI0000176DC8; EMBL:X62956
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:
Pred. No.: 3.54e-40 Length: 119
Score: 515.00 Matches: 104
Percent Similarity: 88.4% Conservative: 3
Best Local Similarity: 86.0% Mismatches: 12
Query Match: 76.9% Indels: 2
DB: 2 Gaps: 1

US-10-679-032-27 (1-363) x S31108 (1-119)

```
Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||:::      ||||||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40
```

```
Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||:::||||||      |||      |||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::   |||
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysAspArg 100

Qy        301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
                          |||   ||||||||||||||||||||||||||||||||||||||||
Db        101 ------ArgLeuThrGlyThrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 118

Qy        361 TCA 363
              |||
Db        119 Ser 119
```

RESULT 2
S31686
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31686
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: UNIPARC:UPI0000116477; EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	4.36e-40	Length:	140
Score:	514.00	Matches:	101
Percent Similarity:	87.6%	Conservative:	5
Best Local Similarity:	83.5%	Mismatches:	15
Query Match:	76.7%	Indels:	0
DB:	2	Gaps:	0

US-10-679-032-27 (1-363) x S31686 (1-140)

```
Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||:::      ||||||||||||||||||||||
Db         40 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 59

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||:::||||||      |||      |||||||||
Db         60 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 79

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              :::||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         80 SerAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 99

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysCysPro 119

Qy        301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
                          :::||||||||||||||||||||||||||||||||||||||||||||
Db        120 PheAlaGlyGlySerProSerPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 139

Qy        361 TCA 363
              |||
Db        140 Ser 140
```

RESULT 3
C36005
Ig heavy chain V region (30p1) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C;Accession: C36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: C36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPARC:UPI0000176C27; GB:M18513
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	6.75e-40	Length:	119
Score:	512.00	Matches:	104
Percent Similarity:	88.4%	Conservative:	3
Best Local Similarity:	86.0%	Mismatches:	12
Query Match:	76.4%	Indels:	2
DB:	2	Gaps:	1

US-10-679-032-27 (1-363) x C36005 (1-119)

```
Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||:::      ||||||||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||:::||||||      |||      |||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysAspAla 100

Qy        301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
                      ||||||      ||||||||||||||||||||||||||||||||||||||||
Db        101 GlyTrpGlySerGly------PheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 118

Qy        361 TCA 363
              |||
Db        119 Ser 119
```

RESULT 4
S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S48798
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S48798
A;Status: preliminary

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:33:44 ; Search time 25.0866 Seconds
(without alignments)
2041.778 Million cell updates/sec

Title: US-10-679-032-27
Perfect score: 670
Sequence: 1 gaggtgcagctgttggagtc.....cactggtcaccgtgagctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122108_13629/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_580_@runat_21032006_122108_13629 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	487	72.7	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
2	482.5	72.0	469	2	Q569F4_HUMAN	Q569f4 homo sapien
3	480	71.6	470	2	Q6PJA4_HUMAN	Q6pja4 homo sapien
4	478.5	71.4	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
5	475	70.9	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
6	474.5	70.8	118	2	Q9UL72_HUMAN	Q9ul72 homo sapien
7	473	70.6	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
8	473	70.6	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien
9	472	70.4	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
10	470	70.1	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
11	468	69.9	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
12	467.5	69.8	122	1	HV3G_HUMAN	P01768 homo sapien
13	467.5	69.8	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
14	467.5	69.8	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
15	467	69.7	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
16	466.5	69.6	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
17	465.5	69.5	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
18	464.5	69.3	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
19	462	69.0	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
20	460.5	68.7	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
21	460	68.7	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
22	459.5	68.6	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien
23	455.5	68.0	122	2	Q9UL84_HUMAN	Q9ul84 homo sapien
24	455	67.9	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculu
25	453	67.6	121	1	HV3J_HUMAN	P01771 homo sapien
26	452.5	67.5	487	2	Q99KA4_MOUSE	Q99ka4 mus musculu
27	452	67.5	131	2	Q9UL88_HUMAN	Q9ul88 homo sapien
28	450.5	67.2	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
29	450	67.2	479	2	Q5BK12_RAT	Q5bk12 rattus norv
30	448.5	66.9	119	2	Q5F2I8_MOUSE	Q5f2i8 mus musculu
31	448	66.9	119	2	Q920E7_MOUSE	Q920e7 mus musculu
32	448	66.9	499	2	Q8N5K4_HUMAN	Q8n5k4 homo sapien
33	446.5	66.6	147	2	Q9Y509_HUMAN	Q9y509 homo sapien
34	445.5	66.5	494	2	Q96K68_HUMAN	Q96k68 homo sapien
35	444	66.3	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
36	443.5	66.2	116	1	HV3T_HUMAN	P01781 homo sapien
37	443	66.1	117	1	HV3C_HUMAN	P01764 homo sapien
38	441.5	65.9	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien
39	441	65.8	493	2	Q8NCL6_HUMAN	Q8ncl6 homo sapien
40	439.5	65.6	122	1	HV3H_HUMAN	P01769 homo sapien
41	439.5	65.6	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien
42	438.5	65.4	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
43	437.5	65.3	114	1	HV3B_HUMAN	P01763 homo sapien
44	436	65.1	119	1	HV3I_HUMAN	P01770 homo sapien
45	435.5	65.0	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv

ALIGNMENTS

RESULT 1
Q96BB9_HUMAN
ID Q96BB9_HUMAN PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

```
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2500644;
RA   Kishimoto T., Okajima H., Okumoto T., Taniguchi M.;
RT   "Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-
RT   chains of a human monoclonal antibody with broad reactivity to
RT   malignant tumor cells.";
RL   Nucleic Acids Res. 17:4385-0(1989).
DR   EMBL; BC015760; AAH15760.1; -; mRNA.
DR   PIR; S05271; S05271.
DR   PIR; S24260; S24260.
DR   HSSP; P01861; 1ADQ.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   597 AA;  65039 MW;  4FCA3AD8ECE263D9 CRC64;

Alignment Scores:
Pred. No.:              1.82e-40        Length:         597
Score:                  487.00          Matches:        99
Percent Similarity:     84.8%           Conservative:   7
Best Local Similarity:  79.2%           Mismatches:     15
Query Match:            72.7%           Indels:         4
DB:                     2               Gaps:           1

US-10-679-032-27 (1-363) x Q96BB9_HUMAN (1-597)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 39

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||:::||||||:::      |||:::||||||||||||||||
Db         40 SerCysAlaAlaSerGlyPheSerPheSerSerTyrAlaMetAsnTrpValArgGlnAla 59

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||:::||||||      |||      |||||||||
Db         60 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 79

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||   ||||||||||||||||||:::::|||||||||
Db         80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerArgAspThrLeuTyr 99

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysAspPro 119

Qy        301 GTGGGTCCGTCCGGCGGGGCC------------TTTGACTACTGGGGCCAGGGTACACTG 348
                 |||   |||                     ||||||||||||||||||||||
Db        120 ArgGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyrTrpGlyGlnGlyThrLeu 139

Qy        349 GTCACCGTGAGCTCA 363
              |||||||||||||||
Db        140 ValThrValSerSer 144

RESULT 2
Q569F4_HUMAN
ID   Q569F4_HUMAN PRELIMINARY;      PRT;   469 AA.
AC   Q569F4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092518; AAH92518.1; -; mRNA.
SQ   SEQUENCE   469 AA;  51254 MW;  AC13448E3047784F CRC64;

Alignment Scores:
Pred. No.:              5e-40           Length:         469
Score:                  482.50          Matches:        98
Percent Similarity:     85.1%           Conservative:   5
Best Local Similarity:  81.0%           Mismatches:     17
Query Match:            72.0%           Indels:         1
DB:                     2               Gaps:           1

US-10-679-032-27 (1-363) x Q569F4_HUMAN (1-469)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||:::||||||||||||   :::||||||||||||||||||||||||||||
Db         20 GluValGlnLeuValGluSerGlyGlyValValValGlnProGlyGlySerLeuArgLeu 39

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||   :::      |||   ||||||||||||||||
Db         40 SerCysAlaAlaSerGlyPheThrPheAspAspTyrAlaMetHisTrpValArgGlnAla 59

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||||   ||||||      |||      |||||||||
Db         60 ProGlyLysGlyLeuGluTrpValSerLeuIleSerTrpAspGlyGlySerThrTyrTyr 79

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||   ||||||||||||||||||||||||||:::||||||
Db         80 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnSerLeuTyr 99

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||||      |||
Db        100 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrTyrCysAla---ThrArg 118

Qy        301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
                 |||   |||          ||||||||||||||||||||||||||||||||||||||||||
Db        119 GlyGlyTyrSerThrAlaGlyPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 138

Qy        361 TCA 363
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:48:45 ; Search time 5.21552 Seconds
(without alignments)
1150.845 Million cell updates/sec

Title: US-10-679-032-27
Perfect score: 670
Sequence: 1 gaggtgcagctgttggagtc.....cactggtcaccgtgagctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122111_13720/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10679032_@CGN_1_1_101_@runat_21032006_122111_13720
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523.5	78.1	122	1	US-07-934-373C-21	Sequence 21, Appl
2	523.5	78.1	122	2	US-08-437-642B-21	Sequence 21, Appl
3	523.5	78.1	122	2	US-08-146-206C-21	Sequence 21, Appl
4	523.5	78.1	122	2	US-09-705-686-21	Sequence 21, Appl
5	523.5	78.1	122	2	US-09-705-392A-21	Sequence 21, Appl
6	523.5	78.1	122	2	US-09-705-398-21	Sequence 21, Appl
7	523.5	78.1	122	4	PCT-US93-07832-21	Sequence 21, Appl
8	522.5	78.0	240	2	US-09-192-854-2	Sequence 2, Appli
9	522.5	78.0	240	2	US-09-511-939-2	Sequence 2, Appli
10	521	77.8	119	1	US-07-988-925-11	Sequence 11, Appl
11	521	77.8	119	1	US-08-362-780-11	Sequence 11, Appl
12	521	77.8	119	2	US-08-478-684G-11	Sequence 11, Appl
13	520	77.6	474	2	US-09-848-832-3	Sequence 3, Appli
14	514	76.7	119	2	US-09-648-067A-15	Sequence 15, Appl
15	514	76.7	119	2	US-09-602-812A-6	Sequence 6, Appli
16	512	76.4	117	2	US-09-025-769B-24	Sequence 24, Appl
17	512	76.4	117	2	US-09-490-070A-24	Sequence 24, Appl
18	512	76.4	117	2	US-09-490-153-24	Sequence 24, Appl
19	512	76.4	117	2	US-09-490-324-24	Sequence 24, Appl
20	509.5	76.0	122	4	PCT-US93-08435-12	Sequence 12, Appl
21	509	76.0	123	2	US-09-840-459-82	Sequence 82, Appl
22	509	76.0	123	2	US-09-497-625A-82	Sequence 82, Appl
23	506.5	75.6	120	2	US-09-025-769B-38	Sequence 38, Appl
24	506.5	75.6	120	2	US-09-025-769B-63	Sequence 63, Appl
25	506.5	75.6	120	2	US-09-490-070A-38	Sequence 38, Appl
26	506.5	75.6	120	2	US-09-490-070A-63	Sequence 63, Appl
27	506.5	75.6	120	2	US-09-490-153-38	Sequence 38, Appl
28	506.5	75.6	120	2	US-09-490-153-63	Sequence 63, Appl
29	506.5	75.6	120	2	US-09-490-324-38	Sequence 38, Appl
30	506.5	75.6	120	2	US-09-490-324-63	Sequence 63, Appl
31	506.5	75.6	122	4	PCT-US93-08435-14	Sequence 14, Appl
32	506.5	75.6	281	2	US-09-025-769B-178	Sequence 178, App
33	506.5	75.6	281	2	US-09-490-070A-178	Sequence 178, App
34	506.5	75.6	281	2	US-09-490-153-178	Sequence 178, App
35	506.5	75.6	281	2	US-09-490-324-178	Sequence 178, App
36	506	75.5	113	2	US-08-974-899-6	Sequence 6, Appli
37	506	75.5	113	2	US-09-795-798-6	Sequence 6, Appli
38	506	75.5	113	2	US-08-908-469-11	Sequence 11, Appl
39	503.5	75.1	122	4	PCT-US93-08435-43	Sequence 43, Appl
40	503.5	75.1	135	2	US-08-579-378A-20	Sequence 20, Appl
41	503.5	75.1	443	4	PCT-US96-13152-4	Sequence 4, Appli
42	502.5	75.0	263	2	US-09-069-821-3	Sequence 3, Appli
43	502.5	75.0	263	2	US-09-956-086-3	Sequence 3, Appli
44	502.5	75.0	263	2	US-09-956-087-3	Sequence 3, Appli
45	502.5	75.0	283	2	US-09-420-592A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-07-934-373C-21
; Sequence 21, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:

```
;      TELEPHONE:  650/225-1994
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-07-934-373C-21

Alignment Scores:
Pred. No.:              2.07e-50        Length:         122
Score:                  523.50          Matches:        106
Percent Similarity:     89.3%           Conservative:   3
Best Local Similarity:  86.9%           Mismatches:     12
Query Match:            78.1%           Indels:         1
DB:                     1               Gaps:           1

US-10-679-032-27 (1-363) x US-07-934-373C-21 (1-122)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||:::      ||||||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              |||||||||||||||||||||||||  ||||||     |||     |||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerValIleSerGlyAspGlyGlySerThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGlyArg 100

Qy        301 GTGGGTCCGTCC---GGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTG 357
              ||||||   |||      |||   :::||||||||||||||||||||||||||||||||
Db        101 ValGlyTyrSerLeuSerGlyLeuTyrAspTyrTrpGlyGlnGlyThrLeuValThrVal 120

Qy        358 AGCTCA 363
              ||||||
Db        121 SerSer 122

RESULT 2
US-08-437-642B-21
; Sequence 21, Application US/08437642B
; Patent No. 6054297
;  GENERAL INFORMATION:
;    APPLICANT:  Paul J. Carter
;    APPLICANT:  Leonard G. Presta
;    TITLE OF INVENTION:  Immunoglobulin Variants
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/437,642B
;      FILING DATE:  09-May-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/934373
;      FILING DATE:  21-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146206
;      FILING DATE:  17-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05126
;      FILING DATE:  15-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/715272
;      FILING DATE:  14-JUN-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lee, Wendy M.
;      REGISTRATION NUMBER:  40,378
;      REFERENCE/DOCKET NUMBER:  P0709P2C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-1994
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-437-642B-21

Alignment Scores:
Pred. No.:              2.07e-50        Length:         122
Score:                  523.50          Matches:        106
Percent Similarity:     89.3%           Conservative:   3
Best Local Similarity:  86.9%           Mismatches:     12
Query Match:            78.1%           Indels:         1
DB:                     2               Gaps:           1

US-10-679-032-27 (1-363) x US-08-437-642B-21 (1-122)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||:::      ||||||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              |||||||||||||||||||||||||  ||||||     |||     |||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerValIleSerGlyAspGlyGlySerThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGlyArg 100

Qy        301 GTGGGTCCGTCC---GGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTG 357
              ||||||   |||      |||   :::||||||||||||||||||||||||||||||||
Db        101 ValGlyTyrSerLeuSerGlyLeuTyrAspTyrTrpGlyGlnGlyThrLeuValThrVal 120

Qy        358 AGCTCA 363
              ||||||
Db        121 SerSer 122

RESULT 3
US-08-146-206C-21
; Sequence 21, Application US/08146206C
; Patent No. 6407213
;  GENERAL INFORMATION:
;    APPLICANT:  Carter, Paul J.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Method for Making Humanized Antibodies
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 20:13:25 ; Search time 17.6284 Seconds
(without alignments)
1720.765 Million cell updates/sec

Title: US-10-679-032-27
Perfect score: 670
Sequence: 1 gaggtgcagctgttggagtc.....cactggtcaccgtgagctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122118_13874/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_405_@runat_21032006_122118_13874 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	527	78.7	224	3	US-09-972-656-68	Sequence 68, Appl
2	523.5	78.1	122	5	US-10-835-641-21	Sequence 21, Appl
3	522.5	78.0	116	4	US-10-409-814A-2	Sequence 2, Appli
4	522.5	78.0	116	5	US-10-744-774-5	Sequence 5, Appli
5	522.5	78.0	240	3	US-09-192-854-2	Sequence 2, Appli
6	522.5	78.0	240	3	US-09-968-561A-2	Sequence 2, Appli
7	522.5	78.0	240	3	US-09-968-744A-2	Sequence 2, Appli
8	522.5	78.0	240	3	US-09-968-561A-2	Sequence 2, Appli
9	522.5	78.0	240	5	US-10-744-774-1	Sequence 1, Appli
10	522.5	78.0	240	6	US-11-115-682-2	Sequence 2, Appli
11	521	77.8	119	4	US-10-743-423B-11	Sequence 11, Appl
12	521	77.8	119	5	US-10-491-112-11	Sequence 11, Appl
13	521	77.8	131	5	US-10-783-311-167	Sequence 167, App
14	521	77.8	131	5	US-10-783-311-191	Sequence 191, App
15	521	77.8	147	5	US-10-916-840-52	Sequence 52, Appl
16	521	77.8	449	3	US-09-736-371B-21	Sequence 21, Appl
17	521	77.8	449	4	US-10-463-442-21	Sequence 21, Appl
18	520	77.6	131	5	US-10-916-840-92	Sequence 92, Appl
19	520	77.6	474	3	US-09-848-832-3	Sequence 3, Appli
20	520	77.6	474	4	US-10-225-108A-3	Sequence 3, Appli
21	520	77.6	474	4	US-10-461-148-1	Sequence 1, Appli
22	518	77.3	250	4	US-10-779-461-8	Sequence 8, Appli
23	516	77.0	123	4	US-10-269-805-59	Sequence 59, Appl
24	516	77.0	138	4	US-10-010-942B-12	Sequence 12, Appl
25	516	77.0	138	4	US-10-388-389-12	Sequence 12, Appl
26	516	77.0	138	4	US-10-703-713-12	Sequence 12, Appl
27	516	77.0	138	4	US-10-704-070-12	Sequence 12, Appl
28	516	77.0	138	5	US-10-232-030-12	Sequence 12, Appl
29	516	77.0	248	6	US-11-017-030-47	Sequence 47, Appl
30	515.5	76.9	132	5	US-10-783-311-87	Sequence 87, Appl
31	515.5	76.9	253	6	US-11-017-030-20	Sequence 20, Appl
32	514.5	76.8	244	6	US-11-090-847-147	Sequence 147, App
33	514	76.7	119	3	US-09-811-123-3	Sequence 3, Appli
34	514	76.7	119	4	US-10-268-501-6	Sequence 6, Appli
35	514	76.7	119	4	US-10-608-626-6	Sequence 6, Appli
36	514	76.7	119	4	US-10-600-152-15	Sequence 15, Appl
37	514	76.7	119	4	US-10-619-754-6	Sequence 6, Appli
38	514	76.7	119	5	US-10-719-310-6	Sequence 6, Appli
39	514	76.7	119	5	US-10-861-049-42	Sequence 42, Appl
40	514	76.7	119	6	US-11-021-874-42	Sequence 42, Appl
41	514	76.7	119	6	US-11-044-749-6	Sequence 6, Appli
42	514	76.7	119	6	US-11-154-465-6	Sequence 6, Appli
43	513.5	76.6	246	4	US-10-779-461-47	Sequence 47, Appl
44	513	76.6	244	4	US-10-322-673-45	Sequence 45, Appl
45	513	76.6	244	5	US-10-981-465-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-09-972-656-68
; Sequence 68, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-68

Alignment Scores:

Pred. No.:	1.55e-41	Length:	224
Score:	527.00	Matches:	104
Percent Similarity:	89.3%	Conservative:	4
Best Local Similarity:	86.0%	Mismatches:	13
Query Match:	78.7%	Indels:	0
DB:	3	Gaps:	0

US-10-679-032-27 (1-363) x US-09-972-656-68 (1-224)

```
Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
```

```
                ||||||||||||||||||||||||||||||:::     ||||||||||||||||||||
Db          21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy         121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
                ||||||||||||||||||||||||||||:::||||||     |||     |||||||||
Db          41 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 60

Qy         181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
                ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db          61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy         241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||:::   |||
Db          81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysAspArg 100

Qy         301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
                ||||||   |||           ||||||||||||||||||||||||||||||||||||
Db         101 ValGlyTyrSerSerSerLeuLeuAspTyrTrpGlyGlnGlyThrLeuValThrValSer 120

Qy         361 TCA 363
                |||
Db         121 Ser 121
```

RESULT 2
US-10-835-641-21
; Sequence 21, Application US/10835641
; Publication No. US20040236078A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/835,641
; FILING DATE: 30-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-Nov-2000
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-835-641-21

Alignment Scores:

Pred. No.:	3.13e-41	Length:	122
Score:	523.50	Matches:	106
Percent Similarity:	89.3%	Conservative:	3
Best Local Similarity:	86.9%	Mismatches:	12
Query Match:	78.1%	Indels:	1
DB:	5	Gaps:	1

US-10-679-032-27 (1-363) x US-10-835-641-21 (1-122)

```
Qy           1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
               ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db           1 GluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy          61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
               ||||||||||||||||||||||||||||||:::     ||||||||||||||||||||
Db          21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy         121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
               |||||||||||||||||||||||||||  ||||||    |||     |||||||||
Db          41 ProGlyLysGlyLeuGluTrpValSerValIleSerGlyAspGlyGlySerThrTyrTyr 60

Qy         181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
               ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db          61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy         241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db          81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgGlyArg 100

Qy         301 GTGGGTCCGTCC---GGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTG 357
               ||||||   |||     |||   :::||||||||||||||||||||||||||||||||
Db         101 ValGlyTyrSerLeuSerGlyLeuTyrAspTyrTrpGlyGlnGlyThrLeuValThrVal 120

Qy         358 AGCTCA 363
               ||||||
Db         121 SerSer 122
```

RESULT 3
US-10-409-814A-2
; Sequence 2, Application US/10409814A
; Publication No. US20040202995A1
; GENERAL INFORMATION:
; APPLICANT: de Wildt, Rudolf
; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND SCREENING METHODS
; FILE REFERENCE: 8039/2032
; CURRENT APPLICATION NUMBER: US/10/409,814A
; CURRENT FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-814A-2

Alignment Scores:

Pred. No.:	3.88e-41	Length:	116
Score:	522.50	Matches:	105
Percent Similarity:	89.3%	Conservative:	3
Best Local Similarity:	86.8%	Mismatches:	8
Query Match:	78.0%	Indels:	5
DB:	4	Gaps:	1

US-10-679-032-27 (1-363) x US-10-409-814A-2 (1-116)

```
Qy           1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy          61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
               ||||||||||||||||||||||||||||||:::     ||||||||||||||||||||
Db          21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy         121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
               ||||||||||||||||||||||||||||:::||||||     |||     |||||||||
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 20:15:00 ; Search time 2.29483 Seconds
(without alignments)
905.524 Million cell updates/sec

Title: US-10-679-032-27
Perfect score: 670
Sequence: 1 gaggtgcagctgttggagtc.....cactggtcaccgtgagctca 363

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122120_13932/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_24_@runat_21032006_122120_13932 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	528.5	78.9	120	6	US-10-925-366A-286	Sequence 286, App
2	522.5	78.0	116	6	US-10-925-366A-1	Sequence 1, Appli
3	522.5	78.0	240	6	US-10-925-366A-219	Sequence 219, App
4	521	77.8	147	7	US-11-049-536-52	Sequence 52, Appl
5	520	77.6	131	7	US-11-049-536-92	Sequence 92, Appl
6	516.5	77.1	122	7	US-11-112-240-6	Sequence 6, Appli
7	516.5	77.1	122	7	US-11-112-304A-6	Sequence 6, Appli
8	516	77.0	123	6	US-10-982-440-59	Sequence 59, Appl
9	516	77.0	138	6	US-10-789-273-12	Sequence 12, Appl
10	515	76.9	119	7	US-11-049-536-370	Sequence 370, App
11	514.5	76.8	120	6	US-10-925-366A-235	Sequence 235, App
12	514	76.7	119	7	US-11-106-820-9	Sequence 9, Appli
13	514	76.7	119	7	US-11-154-337-6	Sequence 6, Appli
14	514	76.7	119	7	US-11-182-908-6	Sequence 6, Appli
15	514	76.7	119	7	US-11-190-364-9	Sequence 9, Appli
16	514	76.7	119	7	US-11-102-120-6	Sequence 6, Appli
17	514	76.7	119	7	US-11-147-780-9	Sequence 9, Appli
18	514	76.7	119	7	US-11-223-361-6	Sequence 6, Appli
19	513.5	76.6	122	6	US-10-515-241-11	Sequence 11, Appl
20	513	76.6	119	7	US-11-049-536-638	Sequence 638, App
21	513	76.6	238	7	US-11-193-561-10	Sequence 10, Appl
22	513	76.6	238	7	US-11-193-771-10	Sequence 10, Appl
23	513	76.6	238	7	US-11-193-789-10	Sequence 10, Appl
24	513	76.6	238	7	US-11-193-806-10	Sequence 10, Appl
25	513	76.6	238	7	US-11-193-857-10	Sequence 10, Appl
26	512	76.4	117	6	US-10-834-397-24	Sequence 24, Appl
27	512	76.4	117	6	US-10-981-356A-6	Sequence 6, Appli
28	512	76.4	117	7	US-11-096-046-6	Sequence 6, Appli
29	512	76.4	121	6	US-10-925-366A-212	Sequence 212, App
30	511.5	76.3	120	7	US-11-049-536-258	Sequence 258, App
31	511	76.3	123	7	US-11-049-536-238	Sequence 238, App
32	511	76.3	123	7	US-11-049-536-378	Sequence 378, App
33	511	76.3	123	7	US-11-049-536-398	Sequence 398, App
34	511	76.3	131	6	US-10-993-543-80	Sequence 80, Appl
35	511	76.3	143	7	US-11-049-536-48	Sequence 48, Appl
36	510.5	76.2	116	7	US-11-127-932-4	Sequence 4, Appli
37	510.5	76.2	116	7	US-11-127-903-4	Sequence 4, Appli
38	510.5	76.2	118	7	US-11-049-536-338	Sequence 338, App
39	510.5	76.2	118	7	US-11-049-536-606	Sequence 606, App
40	510.5	76.2	126	7	US-11-049-536-430	Sequence 430, App
41	510.5	76.2	128	7	US-11-049-536-76	Sequence 76, Appl
42	510	76.1	117	7	US-11-049-536-354	Sequence 354, App
43	510	76.1	121	7	US-11-049-536-346	Sequence 346, App
44	510	76.1	313	7	US-11-000-463-427	Sequence 427, App
45	509.5	76.0	118	7	US-11-049-536-546	Sequence 546, App

ALIGNMENTS

RESULT 1
US-10-925-366A-286
; Sequence 286, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8

```
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 286
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino Acid Sequence of Domain Antibody
US-10-925-366A-286

Alignment Scores:
Pred. No.:              2.97e-45        Length:         120
Score:                  528.50          Matches:        103
Percent Similarity:     89.3%           Conservative:   5
Best Local Similarity:  85.1%           Mismatches:     12
Query Match:            78.9%           Indels:         1
DB:                     6               Gaps:           1

US-10-679-032-27 (1-363) x US-10-925-366A-286 (1-120)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||          ||||||   ||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheGluTrpTyrTrpMetGlyTrpValArgGlnAla 40

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||:::||||||     |||     |||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||:::::::::
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysValLys 100

Qy        301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
              :::|||     |||     ||||||||||||||||||||||||||||||||||||||||
Db        101 LeuGly---GlyGlyProAsnPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 119

Qy        361 TCA 363
              |||
Db        120 Ser 120

RESULT 2
US-10-925-366A-1
; Sequence 1, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-925-366A-1

Alignment Scores:
Pred. No.:              1.18e-44        Length:         116
Score:                  522.50          Matches:        105
Percent Similarity:     89.3%           Conservative:   3
Best Local Similarity:  86.8%           Mismatches:     8
Query Match:            78.0%           Indels:         5
DB:                     6               Gaps:           1

US-10-679-032-27 (1-363) x US-10-925-366A-1 (1-116)

Qy          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeu 20

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAACGCCTGGATGAGCTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||:::     ||||||||||||||||||||
Db         21 SerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrpValArgGlnAla 40

Qy        121 CCAGGGAAGGGGCTGGAGTGGGTCTCAAGTATTAGTGTTGGTGGACATAGGACATATTAT 180
              ||||||||||||||||||||||||||:::||||||     |||     |||||||||
Db         41 ProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyr 60

Qy        181 GCAGATTCCGTGAAGGGCCGGTCCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db         61 AlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyr 80

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACTGCCGTGTATTACTGTGCACGGATACGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         81 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys------ 98

Qy        301 GTGGGTCCGTCCGGCGGGGCCTTTGACTACTGGGGCCAGGGTACACTGGTCACCGTGAGC 360
                      |||   ||||||||||||||||||||||||||||||||||||||||||||||
Db         99 ---------SerTyrGlyAlaPheAspTyrTrpGlyGlnGlyThrLeuValThrValSer 115

Qy        361 TCA 363
              |||
Db        116 Ser 116

RESULT 3
US-10-925-366A-219
; Sequence 219, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:33:19 ; Search time 19.1379 Seconds
(without alignments)
1529.038 Million cell updates/sec

Title: US-10-679-032-28
Perfect score: 632
Sequence: 1 cagtctgtgctgactcagcc.....ccaagctgacggtcctaggt 333

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122106_13617/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_476_@runat_21032006_122106_13617 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	535	84.7	251	5	ABP45200	Abp45200 Human BLy
2	535	84.7	251	7	ADG96027	Adg96027 Single ch
3	532	84.2	251	5	ABP45218	Abp45218 Human BLy
4	532	84.2	251	7	ADG96045	Adg96045 Single ch
5	530	83.9	235	2	AAW88465	Aaw88465 Monoclona
6	530	83.9	235	8	ADR28079	Adr28079 NPB polyp
7	530	83.9	258	5	ABP45254	Abp45254 Human BLy
8	530	83.9	258	7	ADG96081	Adg96081 Single ch
9	528	83.5	258	5	ABP45244	Abp45244 Human BLy
10	528	83.5	258	7	ADG96071	Adg96071 Single ch
11	527	83.4	247	8	ADR28089	Adr28089 NPB polyp
12	526	83.2	111	2	AAW08489	Aaw08489 C6 human
13	524	82.9	111	2	AAW13515	Aaw13515 Anti-mela
14	524	82.9	254	5	ABP45458	Abp45458 Human BLy
15	524	82.9	254	7	ADG96285	Adg96285 Single ch
16	523	82.8	111	2	AAW90281	Aaw90281 Human ant
17	522	82.6	111	2	AAW08492	Aaw08492 C6 human
18	521	82.4	110	9	AEA44960	Aea44960 Apolipopr
19	521	82.4	111	9	ADZ66149	Adz66149 Variable
20	521	82.4	118	9	ADY50078	Ady50078 Endotheli
21	521	82.4	253	5	ABP45357	Abp45357 Human BLy
22	521	82.4	253	7	ADG96184	Adg96184 Single ch
23	521	82.4	254	5	ABP45854	Abp45854 Human BLy
24	521	82.4	254	7	ADG96681	Adg96681 Single ch
25	521	82.4	255	5	AAE20407	Aae20407 Chimeric
26	521	82.4	258	2	AAW08487	Aaw08487 C6 human
27	521	82.4	262	2	AAW97890	Aaw97890 C6.5/218
28	521	82.4	282	5	AAU75161	Aau75161 Amino aci
29	521	82.4	282	6	ABG73149	Abg73149 C6.5/218
30	521	82.4	282	6	ABG73869	Abg73869 C6.5/218
31	520	82.3	109	5	AAO18429	Aao18429 Anti-GD2
32	520	82.3	244	5	ABP45113	Abp45113 Human BLy
33	520	82.3	244	5	ABP45203	Abp45203 Human BLy
34	520	82.3	244	7	ADG96030	Adg96030 Single ch
35	520	82.3	244	7	ADG95940	Adg95940 Single ch
36	520	82.3	248	5	ABP45123	Abp45123 Human BLy
37	520	82.3	248	7	ADG95950	Adg95950 Single ch
38	520	82.3	251	5	ABP45821	Abp45821 Human BLy
39	520	82.3	251	7	ADG96648	Adg96648 Single ch
40	519	82.1	109	4	AAG93616	Aag93616 Human ant
41	519	82.1	109	6	ABO27423	Abo27423 Anti-Rh(D
42	519	82.1	242	2	AAY21881	Aay21881 Amino aci
43	519	82.1	244	2	AAY21883	Aay21883 Amino aci
44	519	82.1	245	8	ADR28087	Adr28087 NPB polyp
45	519	82.1	248	5	ABP45879	Abp45879 Human BLy

ALIGNMENTS

RESULT 1
ABP45200
ID ABP45200 standard; protein; 251 AA.
XX
AC ABP45200;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 1211.
XX
KW BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

```
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan T,  Hilbert D;
XX
DR   WPI; 2002-114799/15.
XX
PT   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT   diagnosis and treatment of cancers and immune disorders.
XX
PS   Claim 1; Page 1847-1848; 3148pp; English.
XX
CC   This invention describes novel antibodies that immunospecifically bind to
CC   B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC   tumour necrosis factor (TNF) super family and induces B cell
CC   proliferation and differentiation. The antibodies of the invention have
CC   cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC   antirheumatic and antiAIDS activity and can be used in vaccines to
CC   inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC   and so may be used to detect and quantitate the presence of BLyS in
CC   biological samples and may be used in this way to diagnose disease
CC   associated with aberrant expression of BLyS. They may also be
CC   administered to treat diseases associated with aberrant BLyS expression
CC   and activity such as cancer, immune, and autoimmune disorders and
CC   diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC   immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC   acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC   the antibodies and fragments of the antibodies described in the method of
CC   the invention
XX
SQ   Sequence 251 AA;

Alignment Scores:
Pred. No.:              1.08e-47        Length:         251
Score:                  535.00          Matches:        100
Percent Similarity:     96.4%           Conservative:   7
Best Local Similarity:  90.1%           Mismatches:     4
Query Match:            84.7%           Indels:         0
DB:                     5               Gaps:           0

US-10-679-032-28 (1-333) x ABP45200 (1-251)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::||||||||    |||   |||:::|||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnLeu 180

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db        181 ProGlyThrAlaProLysLeuLeuIleTyrSerAsnAsnGlnArgProSerGlyValPro 200

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        201 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 220

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||:::||||||   ||||||||||||||||||
Db        221 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyTrpVal 240

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        241 PheGlyGlyGlyThrLysLeuThrValLeuGly 251

RESULT 2
ADG96027
ID   ADG96027 standard; protein; 251 AA.
XX
AC   ADG96027;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Single chain antibody that immunospecifically binds BLyS SeqID 1211.
XX
KW   antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KW   B cell proliferation; differentiation; scFv; myasthenia gravis;
KW   multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW   carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW   antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS   Unidentified.
XX
PN   WO2003055979-A2.
XX
PD   10-JUL-2003.
XX
PF   14-NOV-2002; 2002WO-US036496.
XX
PR   16-NOV-2001; 2001US-0331469P.
PR   19-DEC-2001; 2001US-0340817P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Barash SC,  Choi GH,  Vaughan TJ,  Hilbert D;
XX
DR   WPI; 2003-505530/47.
XX
PT   Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT   (BLys), useful for detecting and treating diseases or disorders e.g.
PT   rheumatoid arthritis, asthma and leukemia.
XX
PS   Example 1; SEQ ID NO 1211; 394pp; English.
XX
CC   This invention relates to novel antibodies that immunospecifically bind
CC   to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to
CC   chromosome 13q34 and encodes a protein that is a member of the tumour
CC   necrosis factor superfamily and induces both in vivo and in vitro B cell
CC   proliferation and differentiation. Specifically, it refers to single
CC   chain antibody molecules (scFvs) derived, preferably, from the variable
CC   heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC   fragment thereof, of either human, murine, rat or monkey BLyS. The
CC   present invention refers to the use of such antibodies in various methods
CC   for the detection, diagnosis and prognosis of diseases related to the
CC   aberrant expression or inappropriate function of BLyS or its receptor. As
CC   such, these compositions are useful for identifying immune disorders
CC   including myasthenia gravis and multiple sclerosis, inflammatory
CC   disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC   as AIDS and proliferative disorders including leukaemia, carcinoma and
CC   lymphoma. Accordingly, they can be described as exhibiting various
CC   activities such as antirheumatic, antiarthritic, neuroprotective,
CC   antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC   polypeptide sequence is a single chain antibody that binds BLyS of the
CC   invention. NOTE: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format
CC   directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ   Sequence 251 AA;

Alignment Scores:
Pred. No.:              1.08e-47        Length:         251
Score:                  535.00          Matches:        100
Percent Similarity:     96.4%           Conservative:   7
Best Local Similarity:  90.1%           Mismatches:     4
Query Match:            84.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-679-032-28 (1-333) x ADG96027 (1-251)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::||||||||    |||   |||:::|||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnLeu 180
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:40:45 ; Search time 4.06681 Seconds
(without alignments)
1575.691 Million cell updates/sec

Title: US-10-679-032-28
Perfect score: 632
Sequence: 1 cagtctgtgctgactcagcc.....ccaagctgacggtcctaggt 333

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122109_13665/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_77_@runat_21032006_122109_13665 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	538	85.1	129	2	S78058	Ig lambda chain pr
2	524	82.9	216	2	A42193	Ig lambda chain (B
3	519	82.1	233	2	S25752	Ig lambda chain -
4	517	81.8	130	2	S78057	Ig lambda chain pr
5	506.5	80.1	149	2	S23626	Ig lambda chain V
6	502	79.4	234	2	S25757	Ig lambda chain -
7	493	78.0	110	2	S57408	Ig lambda chain V-
8	493	78.0	235	2	S25750	Ig lambda chain -
9	490	77.5	112	2	C44151	Ig lambda chain V
10	490	77.5	112	2	D44151	Ig lambda chain V
11	487	77.1	109	1	L1HUWA	Ig lambda chain V-
12	487	77.1	112	2	B44151	Ig lambda chain V
13	485.5	76.8	235	2	S25754	Ig lambda chain -
14	484	76.6	233	2	S25744	Ig lambda chain -
15	483	76.4	130	1	L1HUBL	Ig lambda chain pr
16	482	76.3	111	2	S36274	Ig lambda chain V
17	481	76.1	111	2	S47009	Ig lambda chain V1
18	480	75.9	235	2	S05270	Ig lambda chain pr
19	478	75.6	130	2	S09712	Ig lambda chain V
20	477.5	75.6	236	2	S25746	Ig lambda chain -
21	475	75.2	112	2	A44151	Ig lambda chain V
22	475	75.2	216	2	S03401	Ig lambda chain (K
23	474	75.0	110	2	S57428	Ig light chain V-J
24	470.5	74.4	112	2	S51148	antibody light cha
25	467	73.9	111	1	L1HUVO	Ig lambda chain V-
26	466	73.7	98	2	S36048	Ig lambda chain -
27	463	73.3	98	2	S36047	Ig lambda chain -
28	463	73.3	111	1	L1HUNW	Ig lambda chain V-
29	463	73.3	117	2	S23627	Ig lambda chain pr
30	462	73.1	131	2	S24321	Ig lambda chain pr
31	462	73.1	232	2	S25742	Ig lambda chain -
32	461.5	73.0	112	1	L1HUHA	Ig lambda chain V-
33	461	72.9	111	1	L1HUNG	Ig lambda chain V-
34	459.5	72.7	112	1	L1HUMM	Ig lambda chain V-
35	458	72.5	111	2	S47185	Ig lambda chain -
36	453.5	71.8	217	2	JE0246	Ig lambda chain NI
37	453	71.7	111	2	S19664	Ig lambda chain V
38	452	71.5	113	2	A29700	Ig lambda chain V
39	451	71.4	216	2	S29258	Ig lambda chain V
40	450.5	71.3	213	2	S21066	Ig lambda chain V
41	449	71.0	110	2	S36258	Ig lambda chain V
42	441	69.8	111	2	S36263	Ig lambda chain V
43	432	68.4	109	1	L1HUEP	Ig lambda chain V-
44	430.5	68.1	99	2	S36054	Ig lambda chain -
45	429.5	68.0	99	2	S36053	Ig lambda chain -

ALIGNMENTS

RESULT 1
S78058
Ig lambda chain precursor V-J region (clone mAB 67VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78058; S23723
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78058
A;Molecule type: mRNA
A;Residues: 1-129 <HAR>
A;Cross-references: UNIPARC:UPI0000115E8D; EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkine
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23723
A;Molecule type: mRNA
A;Residues: 19-129 <HAW>
A;Cross-references: UNIPARC:UPI000017683E; EMBL:X54446
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F;19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F;33-109/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	2.9e-37	Length:	129
Score:	538.00	Matches:	101
Percent Similarity:	95.5%	Conservative:	5
Best Local Similarity:	91.0%	Mismatches:	5
Query Match:	85.1%	Indels:	0
DB:	2	Gaps:	0

US-10-679-032-28 (1-333) x S78058 (1-129)

```
Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 38

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::||||||||    ||||||||   ||||||||||||||||
Db         39 SerCysSerGlySerSerSerAsnIleGlySerAsnTyrValTyrTrpTyrGlnGlnLeu 58

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||    |||:::   ||||||||||||||||||
Db         59 ProGlyThrAlaProLysLeuLeuIleTyrArgAsnAsnGlnArgProSerGlyValPro 78

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuArg 98

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||   ||||||:::||||||||
Db         99 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerGlyTrpVal 118

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        119 PheGlyGlyGlyThrLysLeuThrValLeuGly 129
```

RESULT 2
A42193
Ig lambda chain (BJP-DIA) - human
N;Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain (
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C;Accession: A42193; S18297
R;Klafki, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N.
Biochemistry 31, 3265-3272, 1992
A;Title: Complete amino acid sequence determinations demonstrate identity of the urinary
A;Reference number: A42193; MUID:92207944; PMID:1554711
A;Accession: A42193
A;Molecule type: protein
A;Residues: 1-216 <KLA>
A;Cross-references: UNIPARC:UPI0000176B2C
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;131-199/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Alignment Scores:

Pred. No.:	3.97e-36	Length:	216
Score:	524.00	Matches:	97
Percent Similarity:	94.6%	Conservative:	8
Best Local Similarity:	87.4%	Mismatches:	6
Query Match:	82.9%	Indels:	0
DB:	2	Gaps:	0

US-10-679-032-28 (1-333) x A42193 (1-216)

```
Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 20

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::||||||||    |||    |||:::||||||||||||||||
Db         21 SerCysSerGlySerSerSerAsnIleGlySerAsnValValThrTrpTyrGlnGlnLeu 40

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||    |||:::   ||||||||||||||||||
Db         41 ProGlyThrAlaProLysLeuLeuIleTyrThrAsnAsnGlnArgProSerGlyValPro 60

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||:::
Db         61 GlyArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaValSerGlyLeuGln 80

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||   |||:::|||||||||||
Db         81 SerGluAspGluAlaAspTyrTyrCysAlaThrTrpAspAspSerValAsnGlyTrpVal 100

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
```

RESULT 3
S25752
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25752
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25752
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: UNIPARC:UPI0000115F00; EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	1.03e-35	Length:	233
Score:	519.00	Matches:	99
Percent Similarity:	94.6%	Conservative:	6
Best Local Similarity:	89.2%	Mismatches:	6
Query Match:	82.1%	Indels:	0
DB:	2	Gaps:	0

US-10-679-032-28 (1-333) x S25752 (1-233)

```
Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 37

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::||||||||    |||    |||:::||||||||||||||||
Db         38 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnLeu 57

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||    |||:::   ||||||||||||||||||
Db         58 ProGlyThrAlaProLysLeuLeuIleTyrArgAsnAsnGlnArgProSerGlyValPro 77

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         78 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 97

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||   ||||||||||||   |||
Db         98 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyValVal 117

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        118 PheGlyGlyGlyThrLysLeuThrValLeuGly 128
```

RESULT 4
S78057
Ig lambda chain precursor V-J region (clone mAB 61VL) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78057; S23722
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78057
A;Molecule type: mRNA
A;Residues: 1-130 <HAR>
A;Cross-references: UNIPARC:UPI0000115E88; EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:33:44 ; Search time 23.0134 Seconds
(without alignments)
2041.778 Million cell updates/sec

Title: US-10-679-032-28
Perfect score: 632
Sequence: 1 cagtctgtgctgactcagcc.....ccaagctgacggtcctaggt 333

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122108_13629/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_580_@runat_21032006_122108_13629 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	493	78.0	235	2	Q567P1_HUMAN	Q567p1 homo sapien
2	490.5	77.6	236	2	Q8NEJ1_HUMAN	Q8nej1 homo sapien
3	487	77.1	109	1	LV1F_HUMAN	P04208 homo sapien
4	485	76.7	235	2	Q6GMW6_HUMAN	Q6gmw6 homo sapien
5	483	76.4	130	1	LV1G_HUMAN	P06316 homo sapien
6	481.5	76.2	236	2	Q6GMX4_HUMAN	Q6gmx4 homo sapien
7	477	75.5	108	2	Q96SB0_HUMAN	Q96sb0 homo sapien
8	467	73.9	111	1	LV1A_HUMAN	P01699 homo sapien
9	463	73.3	99	2	Q5NV81_HUMAN	Q5nv81 homo sapien
10	463	73.3	111	1	LV1C_HUMAN	P01701 homo sapien
11	463	73.3	237	2	Q6DHW4_HUMAN	Q6dhw4 homo sapien
12	461.5	73.0	112	1	LV1B_HUMAN	P01700 homo sapien
13	461	72.9	111	1	LV1D_HUMAN	P01702 homo sapien
14	459.5	72.7	112	1	LV1H_HUMAN	P06887 homo sapien
15	458	72.5	235	2	Q6IN99_HUMAN	Q6in99 homo sapien
16	456.5	72.2	236	2	Q6GMV7_HUMAN	Q6gmv7 homo sapien
17	456.5	72.2	236	2	Q6GMX3_HUMAN	Q6gmx3 homo sapien
18	453	71.7	110	2	Q8TE63_HUMAN	Q8te63 homo sapien
19	452.5	71.6	236	2	Q96E61_HUMAN	Q96e61 homo sapien
20	432	68.4	109	1	LV1I_HUMAN	P06888 homo sapien
21	429.5	68.0	100	2	Q5NV69_HUMAN	Q5nv69 homo sapien
22	419.5	66.4	236	2	Q6IPQ0_HUMAN	Q6ipq0 homo sapien
23	415	65.7	101	2	Q8IZD8_HUMAN	Q8izd8 homo sapien
24	411	65.0	235	2	Q6PIK1_HUMAN	Q6pik1 homo sapien
25	406	64.2	111	1	LV2G_HUMAN	P01710 homo sapien
26	405	64.1	99	2	Q5NV67_HUMAN	Q5nv67 homo sapien
27	403.5	63.8	233	2	Q6PJA3_HUMAN	Q6pja3 homo sapien
28	399	63.1	97	2	Q5NV70_HUMAN	Q5nv70 homo sapien
29	394.5	62.4	236	2	Q6PIQ7_HUMAN	Q6piq7 homo sapien
30	389	61.6	111	1	LV2F_HUMAN	P01709 homo sapien
31	383	60.6	111	1	LV2C_HUMAN	P01706 homo sapien
32	381	60.3	103	1	LV1E_HUMAN	P01703 homo sapien
33	381	60.3	109	1	LV2E_HUMAN	P01708 homo sapien
34	380.5	60.2	236	2	Q6P5S3_HUMAN	Q6p5s3 homo sapien
35	378	59.8	111	1	LV2I_HUMAN	P01712 homo sapien
36	376.5	59.6	112	1	LV2K_HUMAN	P04209 homo sapien
37	376	59.5	111	1	LV2D_HUMAN	P01707 homo sapien
38	375	59.3	111	1	LV2H_HUMAN	P01711 homo sapien
39	375	59.3	235	2	Q6PJG0_HUMAN	Q6pjg0 homo sapien
40	370	58.5	116	2	Q96JD0_HUMAN	Q96jd0 homo sapien
41	368	58.2	112	2	Q96JD2_HUMAN	Q96jd2 homo sapien
42	367	58.1	111	1	LV2B_HUMAN	P01705 homo sapien
43	364.5	57.7	99	2	Q5NV65_HUMAN	Q5nv65 homo sapien
44	362.5	57.4	110	1	LV2J_HUMAN	P01713 homo sapien
45	357	56.5	233	2	Q8TBC9_HUMAN	Q8tbc9 homo sapien

ALIGNMENTS

RESULT 1
Q567P1_HUMAN
ID Q567P1_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q567P1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGLC2 protein.
GN Name=IGLC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

```
RC   TISSUE=Glandular pool- thyroid;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC093098; AAH93098.1; -; mRNA.
SQ   SEQUENCE   235 AA;  24799 MW;  893C6567F3021DE6 CRC64;

Alignment Scores:
Pred. No.:              5.06e-40       Length:         235
Score:                  493.00         Matches:        92
Percent Similarity:     92.7%          Conservative:   10
Best Local Similarity:  83.6%          Mismatches:     8
Query Match:            78.0%          Indels:         0
DB:                     2              Gaps:           0

US-10-679-032-28 (1-333) x Q567P1_HUMAN (1-235)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db         20 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValProIle 39

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||:::::|||||||||   |||   |||:::||||||||||||
Db         40 SerCysSerGlySerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnPhe 59

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db         60 ProGlyThrAlaProLysLeuLeuIleTyrSerAsnAsnGlnArgProSerGlyValPro 79

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         80 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 99

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              |||||||||:::|||   |||:::||||||:::||||||   :::||||||   ||||||
Db        100 SerGluAspAspAlaValTyrHisCysAlaThrTrpAspAspAsnLeuAsnSerTrpVal 119

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTA 330
              ||||||||||||||||||||||||||||||
Db        120 PheGlyGlyGlyThrLysLeuThrValLeu 129

RESULT 2
Q8NEJ1_HUMAN
ID   Q8NEJ1_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q8NEJ1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC030984; AAH30984.1; -; mRNA.
DR   HSSP; P01703; 7FAB.
DR   SMR; Q8NEJ1; 20-234.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   236 AA;  25024 MW;  1703B77942630E08 CRC64;

Alignment Scores:
Pred. No.:              8.97e-40       Length:         236
Score:                  490.50         Matches:        96
Percent Similarity:     91.0%          Conservative:   5
Best Local Similarity:  86.5%          Mismatches:     9
Query Match:            77.6%          Indels:         1
DB:                     2              Gaps:           1

US-10-679-032-28 (1-333) x Q8NEJ1_HUMAN (1-236)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db         20 GlnSerValLeuThrGlnProProSerAlaSerGlySerProGlyGlnArgValThrIle 39

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||   :::|||||||||   |||||||||   |||||||||||:::
Db         40 SerCysSerGlySerArgSerAsnIleGlySerAsnTyrValTyrTrpTyrGlnGlnVal 59

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||   |||       ||||||||||||||||||
Db         60 ProGlyThrAlaProLysLeuLeuIleTyrArgAsnAspGlnArgProSerGlyValPro 79

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuArg 99

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAAT---GGTTGG 297
              ||||||||||||||||||||||||||||||:::||||||   ||||||:::
Db        100 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuSerValHisVal 119

Qy        298 GTATTCGGCGGAGGAACCAAGCTGACGGTCCTA 330
              ||||||||||||||||||||||||||||||||
Db        120 ValPheGlyGlyGlyThrLysLeuThrValLeu 130

RESULT 3
LV1F_HUMAN
ID   LV1F_HUMAN     STANDARD;      PRT;   109 AA.
AC   P04208;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig lambda chain V-I region WAH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=83221661; PubMed=6407018;
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 19:48:45 ; Search time 4.78448 Seconds
(without alignments)
1150.845 Million cell updates/sec

Title: US-10-679-032-28
Perfect score: 632
Sequence: 1 cagtctgtgctgactcagcc.....ccaagctgacggtcctaggt 333

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122111_13720/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10679032_@CGN_1_1_101_@runat_21032006_122111_13720
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	526	83.2	111	1	US-08-665-202-40	Sequence 40, Appl
2	526	83.2	111	2	US-09-315-574-40	Sequence 40, Appl
3	524	82.9	111	2	US-08-983-607-23	Sequence 23, Appl
4	523	82.8	111	2	US-09-424-840B-8	Sequence 8, Appli
5	522	82.6	111	1	US-08-665-202-43	Sequence 43, Appl
6	522	82.6	111	2	US-09-315-574-43	Sequence 43, Appl
7	521	82.4	111	1	US-08-665-202-36	Sequence 36, Appl
8	521	82.4	111	2	US-09-315-574-36	Sequence 36, Appl
9	521	82.4	258	1	US-08-665-202-5	Sequence 5, Appli
10	521	82.4	258	2	US-09-315-574-5	Sequence 5, Appli
11	521	82.4	262	2	US-09-069-821-4	Sequence 4, Appli
12	521	82.4	262	2	US-09-956-086-4	Sequence 4, Appli
13	521	82.4	262	2	US-09-956-087-4	Sequence 4, Appli
14	521	82.4	282	2	US-09-420-592A-7	Sequence 7, Appli
15	521	82.4	282	2	US-09-985-442-7	Sequence 7, Appli
16	521	82.4	282	2	US-09-983-580-7	Sequence 7, Appli
17	519	82.1	109	2	US-09-240-274-59	Sequence 59, Appl
18	519	82.1	109	2	US-09-848-798-59	Sequence 59, Appl
19	513	81.2	112	2	US-09-025-769B-18	Sequence 18, Appl
20	513	81.2	112	2	US-09-490-070A-18	Sequence 18, Appl
21	513	81.2	112	2	US-09-490-153-18	Sequence 18, Appl
22	513	81.2	112	2	US-09-490-324-18	Sequence 18, Appl
23	512.5	81.1	112	1	US-08-665-202-39	Sequence 39, Appl
24	512.5	81.1	112	2	US-09-315-574-39	Sequence 39, Appl
25	506	80.1	111	1	US-08-665-202-42	Sequence 42, Appl
26	506	80.1	111	2	US-09-315-574-42	Sequence 42, Appl
27	505	79.9	113	1	US-08-211-202-113	Sequence 113, App
28	501	79.3	111	1	US-08-665-202-41	Sequence 41, Appl
29	501	79.3	111	2	US-09-315-574-41	Sequence 41, Appl
30	500	79.1	111	1	US-08-264-093-6	Sequence 6, Appli
31	498	78.8	111	2	US-08-983-607-21	Sequence 21, Appl
32	492	77.8	109	2	US-09-240-274-57	Sequence 57, Appl
33	492	77.8	109	2	US-09-848-798-57	Sequence 57, Appl
34	491	77.7	110	2	US-09-240-274-60	Sequence 60, Appl
35	491	77.7	110	2	US-09-848-798-60	Sequence 60, Appl
36	491	77.7	113	1	US-08-211-202-114	Sequence 114, App
37	486	76.9	109	2	US-09-240-274-55	Sequence 55, Appl
38	486	76.9	109	2	US-09-848-798-55	Sequence 55, Appl
39	486	76.9	235	2	US-09-049-672A-12	Sequence 12, Appl
40	483	76.4	113	1	US-08-211-202-112	Sequence 112, App
41	477.5	75.6	236	2	US-09-049-672A-7	Sequence 7, Appli
42	476	75.3	109	2	US-09-240-274-180	Sequence 180, App
43	476	75.3	109	2	US-09-848-798-180	Sequence 180, App
44	475	75.2	111	1	US-08-107-669D-4	Sequence 4, Appli
45	475	75.2	111	1	US-08-472-788A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-665-202-40
; Sequence 40, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410

```
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-665-202-40

Alignment Scores:
Pred. No.:              9.62e-49        Length:         111
Score:                  526.00          Matches:        97
Percent Similarity:     92.8%           Conservative:   6
Best Local Similarity:  87.4%           Mismatches:     8
Query Match:            83.2%           Indels:         0
DB:                     1               Gaps:           0

US-10-679-032-28 (1-333) x US-08-665-202-40 (1-111)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||   |||      |||||||||:::|||||||||
Db          1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||:::|||:::|||||||||   ||||||||||||||||||||||||||||
Db         21 SerCysSerGlyThrAsnSerAsnIleGlyAlaAsnTyrValSerTrpTyrGlnGlnLeu 40

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||   |||      |||||||||||||||||||
Db         41 ProGlyThrAlaProLysLeuLeuIleTyrThrAsnAspGlnArgProSerGlyValPro 60

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 80

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||:::||||||   |||||||||||||||:::
Db         81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyTrpMet 100

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111

RESULT 2
US-09-315-574-40
; Sequence 40, Application US/09315574
; Patent No. 6512097
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, James D.
;    APPLICANT:  Schier, Robert
;    TITLE OF INVENTION:  No. 6512097el High Affinity Human Antibodies to
;    TITLE OF INVENTION:  Tumor Antigens
;    NUMBER OF SEQUENCES:  141
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Majestic, Parsons, Siebert & Hsue P.C.
;      STREET:  Four Embarcadero Center, Suite 1100
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-4106
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/315,574
;      FILING DATE:  20-MAY-99
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,238
;      FILING DATE:  14-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,250
;      FILING DATE:  15-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/665,202
;      FILING DATE:  13-JUN-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  02307E-061411
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-315-574-40

Alignment Scores:
Pred. No.:              9.62e-49        Length:         111
Score:                  526.00          Matches:        97
Percent Similarity:     92.8%           Conservative:   6
Best Local Similarity:  87.4%           Mismatches:     8
Query Match:            83.2%           Indels:         0
DB:                     2               Gaps:           0

US-10-679-032-28 (1-333) x US-09-315-574-40 (1-111)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||   |||      |||||||||:::|||||||||
Db          1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnLysValThrIle 20

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||:::|||:::|||||||||   ||||||||||||||||||||||||||||
Db         21 SerCysSerGlyThrAsnSerAsnIleGlyAsnAsnTyrValSerTrpTyrGlnGlnLeu 40

Qy        121 CCAGGAACGGCCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||   |||      |||||||||||||||||||
Db         41 ProGlyThrAlaProLysLeuLeuIleTyrThrAsnAspGlnArgProSerGlyValPro 60

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         61 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 80

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||:::||||||   |||||||||||||||:::
Db         81 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyTrpMet 100

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111

RESULT 3
US-08-983-607-23
; Sequence 23, Application US/08983607
; Patent No. 6140470
;  GENERAL INFORMATION:
;    APPLICANT:  Alan Garen
;    APPLICANT:  Xiaohong Cai
;    TITLE OF INVENTION:  Human Anti-Tumor Monoclonal Anti-
;    TITLE OF INVENTION:  bodies
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Department of Molecular Biophysics
;      ADDRESSEE:  and Biochemistry, Yale University
;      STREET:  266 Whitney Avenue
;      CITY:  New Haven
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 20:13:25 ; Search time 16.1716 Seconds
(without alignments)
1720.765 Million cell updates/sec

Title: US-10-679-032-28
Perfect score: 632
Sequence: 1 cagtctgtgctgactcagcc.....ccaagctgacggtcctaggt 333

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/absa/ABSSWEB_spool/US10679032/runat_21032006_122118_13874/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=absa02p
-USER=US10679032_@CGN_1_1_405_@runat_21032006_122118_13874 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	535	84.7	251	3	US-09-880-748-1211	Sequence 1211, Ap
2	535	84.7	251	4	US-10-293-418-1211	Sequence 1211, Ap
3	532	84.2	251	3	US-09-880-748-1229	Sequence 1229, Ap
4	532	84.2	251	4	US-10-293-418-1229	Sequence 1229, Ap
5	530	83.9	235	3	US-09-747-669-6	Sequence 6, Appli
6	530	83.9	235	4	US-10-290-703-6	Sequence 6, Appli
7	530	83.9	258	3	US-09-880-748-1265	Sequence 1265, Ap
8	530	83.9	258	4	US-10-293-418-1265	Sequence 1265, Ap
9	529	83.7	254	6	US-11-090-847-115	Sequence 115, App
10	528	83.5	258	3	US-09-880-748-1255	Sequence 1255, Ap
11	528	83.5	258	4	US-10-293-418-1255	Sequence 1255, Ap
12	524	82.9	254	3	US-09-880-748-1469	Sequence 1469, Ap
13	524	82.9	254	4	US-10-293-418-1469	Sequence 1469, Ap
14	523	82.8	111	4	US-10-844-424-8	Sequence 8, Appli
15	521	82.4	118	5	US-10-916-758-26	Sequence 26, Appl
16	521	82.4	253	3	US-09-880-748-1368	Sequence 1368, Ap
17	521	82.4	253	4	US-10-293-418-1368	Sequence 1368, Ap
18	521	82.4	254	3	US-09-880-748-1865	Sequence 1865, Ap
19	521	82.4	254	4	US-10-293-418-1865	Sequence 1865, Ap
20	521	82.4	255	3	US-09-888-721-34	Sequence 34, Appl
21	521	82.4	262	3	US-09-956-086-4	Sequence 4, Appli
22	521	82.4	262	3	US-09-956-087-4	Sequence 4, Appli
23	521	82.4	282	3	US-09-983-580-7	Sequence 7, Appli
24	521	82.4	282	3	US-09-985-442-7	Sequence 7, Appli
25	520	82.3	244	3	US-09-880-748-1124	Sequence 1124, Ap
26	520	82.3	244	3	US-09-880-748-1214	Sequence 1214, Ap
27	520	82.3	244	4	US-10-293-418-1124	Sequence 1124, Ap
28	520	82.3	244	4	US-10-293-418-1214	Sequence 1214, Ap
29	520	82.3	248	3	US-09-880-748-1134	Sequence 1134, Ap
30	520	82.3	248	4	US-10-293-418-1134	Sequence 1134, Ap
31	520	82.3	251	3	US-09-880-748-1832	Sequence 1832, Ap
32	520	82.3	251	4	US-10-293-418-1832	Sequence 1832, Ap
33	519	82.1	109	3	US-09-848-798-59	Sequence 59, Appl
34	519	82.1	248	3	US-09-880-748-1890	Sequence 1890, Ap
35	519	82.1	248	4	US-10-293-418-1890	Sequence 1890, Ap
36	519	82.1	269	3	US-09-888-721-36	Sequence 36, Appl
37	519	82.1	282	3	US-09-888-721-38	Sequence 38, Appl
38	519	82.1	287	3	US-09-888-721-40	Sequence 40, Appl
39	519	82.1	291	3	US-09-888-721-44	Sequence 44, Appl
40	519	82.1	296	3	US-09-888-721-42	Sequence 42, Appl
41	518	82.0	253	4	US-10-120-414-76	Sequence 76, Appl
42	518	82.0	253	5	US-10-992-195-76	Sequence 76, Appl
43	518	82.0	260	5	US-10-935-290-116	Sequence 116, App
44	517	81.8	251	3	US-09-880-748-1011	Sequence 1011, Ap
45	517	81.8	251	3	US-09-880-748-1542	Sequence 1542, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1211
; Sequence 1211, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1211
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1211

Alignment Scores:

Pred. No.:	3.6e-44	Length:	251
Score:	535.00	Matches:	100
Percent Similarity:	96.4%	Conservative:	7
Best Local Similarity:	90.1%	Mismatches:	4
Query Match:	84.7%	Indels:	0
DB:	3	Gaps:	0

```
US-10-679-032-28 (1-333) x US-09-880-748-1211 (1-251)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::|||||||||   |||   |||:::|||||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnLeu 180

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db        181 ProGlyThrAlaProLysLeuLeuIleTyrSerAsnAsnGlnArgProSerGlyValPro 200

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        201 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 220

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||   ||||||||||||||||||
Db        221 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyTrpVal 240

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        241 PheGlyGlyGlyThrLysLeuThrValLeuGly 251

RESULT 2
US-10-293-418-1211
; Sequence 1211, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P2
;  CURRENT APPLICATION NUMBER: US/10/293,418
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-16
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1211
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-418-1211

Alignment Scores:
Pred. No.:              3.6e-44       Length:          251
Score:                  535.00        Matches:         100
Percent Similarity:     96.4%         Conservative:    7
Best Local Similarity:  90.1%         Mismatches:      4
Query Match:            84.7%         Indels:          0
DB:                     4             Gaps:            0

US-10-679-032-28 (1-333) x US-10-293-418-1211 (1-251)

 y          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::|||||||||   |||   |||:::|||||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnLeu 180

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db        181 ProGlyThrAlaProLysLeuLeuIleTyrSerAsnAsnGlnArgProSerGlyValPro 200

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        201 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 220

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||   ||||||||||||||||||
Db        221 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyTrpVal 240

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        241 PheGlyGlyGlyThrLysLeuThrValLeuGly 251

RESULT 3
US-09-880-748-1229
; Sequence 1229, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523
;  CURRENT APPLICATION NUMBER: US/09/880,748
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 60/212,210
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 3239
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1229
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-880-748-1229

Alignment Scores:
Pred. No.:              7.13e-44      Length:          251
Score:                  532.00        Matches:         100
Percent Similarity:     93.7%         Conservative:    4
Best Local Similarity:  90.1%         Mismatches:      7
Query Match:            84.2%         Indels:          0
DB:                     3             Gaps:            0

US-10-679-032-28 (1-333) x US-09-880-748-1229 (1-251)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::|||||||||   |||   ||||||||||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValSerTrpTyrGlnGlnLeu 180

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||   |||      ||||||||||||||||||
Db        181 ProGlyThrAlaProLysLeuLeuIleTyrThrAsnAspGlnArgProSerGlyValPro 200

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 21, 2006, 20:15:00 ; Search time 2.10517 Seconds
(without alignments)
905.524 Million cell updates/sec

Title: US-10-679-032-28
Perfect score: 632
Sequence: 1 cagtctgtgctgactcagcc.....ccaagctgacggtcctaggt 333

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 339260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679032/runat_21032006_122120_13932/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10679032_@CGN_1_1_24_@runat_21032006_122120_13932 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	535	84.7	251	7	US-11-054-515-1211	Sequence 1211, Ap
2	532	84.2	251	7	US-11-054-515-1229	Sequence 1229, Ap
3	530	83.9	258	7	US-11-054-515-1265	Sequence 1265, Ap
4	528	83.5	258	7	US-11-054-515-1255	Sequence 1255, Ap
5	524	82.9	254	7	US-11-054-515-1469	Sequence 1469, Ap
6	521	82.4	253	7	US-11-054-515-1368	Sequence 1368, Ap
7	521	82.4	254	7	US-11-054-515-1865	Sequence 1865, Ap
8	520	82.3	244	7	US-11-054-515-1124	Sequence 1124, Ap
9	520	82.3	244	7	US-11-054-515-1214	Sequence 1214, Ap
10	520	82.3	248	7	US-11-054-515-1134	Sequence 1134, Ap
11	520	82.3	251	7	US-11-054-515-1832	Sequence 1832, Ap
12	519	82.1	109	7	US-11-064-174-59	Sequence 59, Appl
13	519	82.1	248	7	US-11-054-515-1890	Sequence 1890, Ap
14	517	81.8	251	7	US-11-054-515-1011	Sequence 1011, Ap
15	517	81.8	251	7	US-11-054-515-1542	Sequence 1542, Ap
16	515	81.5	246	7	US-11-054-515-1369	Sequence 1369, Ap
17	514	81.3	244	7	US-11-054-515-1524	Sequence 1524, Ap
18	513	81.2	112	6	US-10-834-397-18	Sequence 18, Appl
19	513	81.2	250	7	US-11-054-515-1222	Sequence 1222, Ap
20	511	80.9	244	7	US-11-054-515-1210	Sequence 1210, Ap
21	511	80.9	244	7	US-11-054-515-1507	Sequence 1507, Ap
22	511	80.9	257	7	US-11-054-515-1553	Sequence 1553, Ap
23	509	80.5	122	6	US-10-993-543-46	Sequence 46, Appl
24	509	80.5	256	7	US-11-054-515-2119	Sequence 2119, Ap
25	508	80.4	122	6	US-10-993-543-110	Sequence 110, App
26	508	80.4	249	7	US-11-054-515-1986	Sequence 1986, Ap
27	507	80.2	252	7	US-11-054-515-1223	Sequence 1223, Ap
28	505.5	80.0	111	7	US-11-112-240-24	Sequence 24, Appl
29	505.5	80.0	111	7	US-11-112-304A-24	Sequence 24, Appl
30	505	79.9	250	7	US-11-054-515-1529	Sequence 1529, Ap
31	505	79.9	251	7	US-11-054-515-1591	Sequence 1591, Ap
32	504	79.7	256	7	US-11-054-515-1253	Sequence 1253, Ap
33	503	79.6	248	7	US-11-054-515-1037	Sequence 1037, Ap
34	503	79.6	250	7	US-11-054-515-1203	Sequence 1203, Ap
35	502	79.4	240	7	US-11-054-515-2045	Sequence 2045, Ap
36	502	79.4	248	7	US-11-054-515-1963	Sequence 1963, Ap
37	502	79.4	249	7	US-11-054-515-1347	Sequence 1347, Ap
38	501	79.3	244	7	US-11-054-515-1491	Sequence 1491, Ap
39	501	79.3	247	7	US-11-054-515-1527	Sequence 1527, Ap
40	501	79.3	249	7	US-11-054-515-1971	Sequence 1971, Ap
41	501	79.3	250	7	US-11-054-515-1228	Sequence 1228, Ap
42	500	79.1	240	7	US-11-054-515-2030	Sequence 2030, Ap
43	499	79.0	244	7	US-11-054-515-1582	Sequence 1582, Ap
44	499	79.0	248	7	US-11-054-515-2091	Sequence 2091, Ap
45	499	79.0	258	7	US-11-054-515-1042	Sequence 1042, Ap

ALIGNMENTS

RESULT 1
US-11-054-515-1211
; Sequence 1211, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1211

```
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1211

Alignment Scores:
Pred. No.:              7.09e-44        Length:         251
Score:                  535.00          Matches:        100
Percent Similarity:     96.4%           Conservative:   7
Best Local Similarity:  90.1%           Mismatches:     4
Query Match:            84.7%           Indels:         0
DB:                     7               Gaps:           0

US-10-679-032-28 (1-333) x US-11-054-515-1211 (1-251)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::|||||||||   |||   |||:::|||||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValAsnTrpTyrGlnGlnLeu 180

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||:::|||:::   ||||||||||||||||||
Db        181 ProGlyThrAlaProLysLeuLeuIleTyrSerAsnAsnGlnArgProSerGlyValPro 200

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        201 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 220

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||   ||||||||||||||||||
Db        221 SerGluAspGluAlaAspTyrTyrCysAlaAlaTrpAspAspSerLeuAsnGlyTrpVal 240

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        241 PheGlyGlyGlyThrLysLeuThrValLeuGly 251

RESULT 2
US-11-054-515-1229
; Sequence 1229, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1229
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1229

Alignment Scores:
Pred. No.:              1.37e-43        Length:         251
Score:                  532.00          Matches:        100
Percent Similarity:     93.7%           Conservative:   4
Best Local Similarity:  90.1%           Mismatches:     7
Query Match:            84.2%           Indels:         0
DB:                     7               Gaps:           0

US-10-679-032-28 (1-333) x US-11-054-515-1229 (1-251)

Qy          1 CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGGCAGAGGGTCACCATC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GlnSerValLeuThrGlnProProSerAlaSerGlyThrProGlyGlnArgValThrIle 160

Qy         61 TCCTGCTCTGGAAGCAACACCAACATTGGGAAGAACTATGTATCTTGGTATCAGCAGCTC 120
              ||||||||||||||::::::|||||||||   |||   |||||||||||||||||||||
Db        161 SerCysSerGlySerSerSerAsnIleGlySerAsnThrValSerTrpTyrGlnGlnLeu 180

Qy        121 CCAGGAACGGCCCCCAAACTCCTCATCTATGCTAATAGCAATCGGCCCTCAGGGGTCCCT 180
              ||||||||||||||||||||||||||||||   |||      ||||||||||||||||||
Db        181 ProGlyThrAlaProLysLeuLeuIleTyrThrAsnAspGlnArgProSerGlyValPro 200

Qy        181 GACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        201 AspArgPheSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuGln 220

Qy        241 TCCGAGGATGAGGCTGATTATTACTGTGCGTCATGGGATGCCAGCCTGAATGGTTGGGTA 300
              ||||||||||||||||||||||||||||||:::||||||     ||||||||||||||||
Db        221 SerGluAspGluAlaAspTyrTyrCysAlaThrTrpAspAspGlyLeuAsnGlyTrpVal 240

Qy        301 TTCGGCGGAGGAACCAAGCTGACGGTCCTAGGT 333
              |||||||||||||||||||||||||||||||
Db        241 PheGlyGlyGlyThrLysLeuThrValLeuGly 251

RESULT 3
US-11-054-515-1265
; Sequence 1265, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1265
;   LENGTH: 258
;   TYPE: PRT
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 18:48:38 ; Search time 188 Seconds
(without alignments)
46.742 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	20	6	AAE34006	Aae34006 Human apo
2	102	100.0	20	8	ADN00563	Adn00563 Apolipopr
3	102	100.0	20	8	ADM98203	Adm98203 Apolipopr
4	102	100.0	809	2	AAY09371	Aay09371 Human apo
5	102	100.0	1671	2	AAR06341	Aar06341 Signal pe
6	102	100.0	2721	1	AAP70647	Aap70647 Sequence
7	102	100.0	3923	2	AAY31237	Aay31237 Human Apo
8	102	100.0	4536	2	AAW41262	Aaw41262 Apolipopr
9	102	100.0	4536	2	AAW96826	Aaw96826 Amino aci
10	102	100.0	4560	5	AAU98981	Aau98981 Human apo
11	102	100.0	4561	7	ADD48677	Add48677 Human Pro
12	102	100.0	4563	5	AAO15893	Aao15893 Human apo
13	102	100.0	4563	6	ABR40253	Abr40253 Human ali
14	102	100.0	4563	6	ABU79140	Abu79140 Apolipopr
15	102	100.0	4563	7	ADF43408	Adf43408 Apolipopr
16	102	100.0	4563	8	ADH18870	Adh18870 Human apo
17	102	100.0	4563	8	ADO33445	Ado33445 Human apo
18	102	100.0	4563	8	ADQ39625	Adq39625 Human myo
19	102	100.0	4563	8	ADQ39624	Adq39624 Human myo
20	102	100.0	4563	9	ADV35127	Adv35127 Human apo
21	102	100.0	4563	9	ADX57616	Adx57616 Rheumatoi
22	102	100.0	4563	9	ADX69305	Adx69305 Human hep
23	102	100.0	4563	9	AEA03079	Aea03079 Apolipopr
24	102	100.0	4590	4	AAU33184	Aau33184 Novel hum
25	95	93.1	4563	8	ADH18871	Adh18871 Human apo
26	95	93.1	4563	8	ADO33447	Ado33447 Human apo
27	58	56.9	178	8	ADS97481	Ads97481 Apolipopr
28	49	48.0	520	4	AAU41718	Aau41718 Propionib
29	49	48.0	520	6	ABM38237	Abm38237 Propionib
30	48	47.1	383	9	ABM97291	Abm97291 M. xanthu
31	48	47.1	987	8	ADR86470	Adr86470 Aspergill
32	47.5	46.6	445	6	ABO14758	Abo14758 Novel hum
33	47.5	46.6	445	6	ABO14759	Abo14759 Novel hum
34	47.5	46.6	445	7	ADM05044	Adm05044 Human pro
35	47.5	46.6	445	8	ADQ39801	Adq39801 Human myo
36	47.5	46.6	445	8	ADR75223	Adr75223 Human gas
37	47.5	46.6	445	9	AEA20143	Aea20143 Novel hum
38	47	46.1	263	7	ABO66068	Abo66068 Klebsiell
39	47	46.1	403	6	ABU03038	Abu03038 Moss lipi
40	47	46.1	403	6	ABU03035	Abu03035 Moss lipi
41	47	46.1	431	7	ADC46639	Adc46639 Thalecres
42	47	46.1	431	7	ADE37253	Ade37253 Plant yie
43	47	46.1	431	8	ADI41579	Adi41579 Plant tra
44	47	46.1	431	8	ADO01759	Ado01759 Thalecres
45	46.5	45.6	154	8	ADX95374	Adx95374 Plant ful

ALIGNMENTS

RESULT 1
AAE34006
ID AAE34006 standard; peptide; 20 AA.
XX
AC AAE34006;
XX
DT 02-MAY-2003 (first entry)
XX
DE Human apo-lipoprotein B peptide #32.
XX
KW Human; immunostimulant; apo-lipoprotein B; apoB; myocardial infarction;
KW vaccine; ischaemic cardiovascular disease; inflammation; cell toxicity;
KW atherosclerosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200280954-A1.
XX
PD 17-OCT-2002.
XX
PF 05-APR-2002; 2002WO-SE000679.
XX
PR 05-APR-2001; 2001SE-00001232.
PR 09-NOV-2001; 2001SE-00003754.
XX
PA (FORS-) FORSKARPATENT I SYD.
XX
PI Nilsson J, Shah PK;
XX
DR WPI; 2003-140132/13.
XX
PT New fragments of apo-lipoprotein B, useful for treatment, prevention and
PT diagnosis of ischemic cardiovascular disease and atherosclerosis.
XX
PS Claim 4; Page 33; 60pp; English.
XX
CC The invention relates to fragments of human apo-lipoprotein B (apoB).
CC ApoB peptides are useful for immunisation or treatment of ischaemic
CC cardiovascular diseases and for diagnosing the presence or absence of
CC antibodies related to increased or decreased risk of developing
CC cardiovascular diseases. They are useful for treating myocardial
CC infarction and unstable atherosclerotic plaques in which oxidised low-
CC density lipoprotein may contribute to inflammation, cell toxicity and
CC risk of plaque rupture. They are also useful as vaccines. The present
CC sequence is human apoB peptide
XX
SQ Sequence 20 AA;

```
  Query Match             100.0%;  Score 102;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 2
ADN00563
ID   ADN00563 standard; peptide; 20 AA.
XX
AC   ADN00563;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Apolipoprotein B oxidised peptide fragment.
XX
KW   human antibody; antibody; apolipoprotein B; atherosclerosis;
KW   passive immunisation; antiarteriosclerotic;
KW   anti-apolipoprotein B antibody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004030698-A1.
XX
PD   15-APR-2004.
XX
PF   22-SEP-2003; 2003WO-SE001469.
XX
PR   04-OCT-2002; 2002SE-00002959.
PR   27-AUG-2003; 2003SE-00002312.
XX
PA   (FORS-) FORSKARPATENT I SYD AB.
XX
PI   Nilsson J,  Carlsson R,  Bengtsson J,  Strandberg L;
XX
DR   WPI; 2004-316343/29.
XX
PT   Use of a recombinant human antibody or antibody fragment directed towards
PT   at least one oxidized fragment of apolipoprotein B for the manufacture of
PT   a pharmaceutical composition for treating atherosclerosis.
XX
PS   Claim 2; Page 26; 59pp; English.
XX
CC   The present invention describes the use of at least one recombinant human
CC   antibody or antibody fragment directed towards at least one oxidised
CC   fragment of apolipoprotein B in the manufacture of a pharmaceutical
CC   composition for treatment of atherosclerosis by means of passive
CC   immunisation. Also described: (1) preparing the isolated antibody; (2)
CC   amplification of isolated human antibody; (3) passive immunisation of
CC   mammals; and (4) a pharmaceutical composition comprising the recombinant
CC   human antibody directed towards at least one oxidised fragment of
CC   apolipoprotein B for treatment of atherosclerosis by means of passive
CC   immunisation. The human antibody has antiarteriosclerotic activity. The
CC   isolated human antibody or antibody fragment directed towards at least
CC   one oxidised fragment of apolipoprotein B is useful in the manufacture of
CC   a pharmaceutical composition for treatment of atherosclerosis by means of
CC   passive immunisation. The present sequence represents an oxidised
CC   fragment of apolipoprotein B, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 102;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 3
ADM98203
ID   ADM98203 standard; peptide; 20 AA.
XX
AC   ADM98203;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Apolipoprotein B oxidised peptide fragment.
XX
KW   human antibody; antibody; apolipoprotein B; atherosclerosis;
KW   passive immunisation; antiarteriosclerotic.
XX
OS   Homo sapiens.
XX
PN   WO2004030607-A2.
XX
PD   15-APR-2004.
XX
PF   06-OCT-2003; 2003WO-SE001547.
XX
PR   04-OCT-2002; 2002SE-00002959.
PR   27-AUG-2003; 2003SE-00002312.
PR   22-SEP-2003; 2003WO-SE001469.
XX
PA   (FORS-) FORSKARPATENT I SYD AB.
XX
PI   Nilsson J,  Carlsson R,  Bengtsson J,  Strandberg L;
XX
DR   WPI; 2004-316320/29.
XX
PT   Use of an isolated human antibody or antibody fragment directed towards
PT   at least one oxidized fragment of apolipoprotein B in the manufacture of
PT   a pharmaceutical composition for treating atherosclerosis.
XX
PS   Claim 2; Page 26; 84pp; English.
XX
CC   The present invention describes the use of at least one isolated human
CC   antibody or antibody fragment directed towards at least one oxidised
CC   fragment of apolipoprotein B in the manufacture of a pharmaceutical
CC   composition for treatment of atherosclerosis by means of passive
CC   immunisation. Also described: (1) preparing the isolated antibody; (2)
CC   amplifying the isolated human antibody; (3) passive immunisation of
CC   mammals; and (4) a pharmaceutical composition comprising the isolated
CC   human antibody directed towards at least one oxidised fragment of
CC   apolipoprotein B for treatment of atherosclerosis by means of passive
CC   immunisation, where the antibody is present in combination with a
CC   pharmaceutical excipient. The human antibody has antiarteriosclerotic
CC   activity. The isolated human antibody or antibody fragment directed
CC   towards at least one oxidised fragment of apolipoprotein B is useful in
CC   the manufacture of a pharmaceutical composition for treatment of
CC   atherosclerosis by means of passive immunisation. The present sequence
CC   represents an oxidised apolipoprotein B peptide fragment, which is used
CC   in the exemplification of the present invention.
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 102;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 4
AAY09371
ID   AAY09371 standard; protein; 809 AA.
XX
```

```
AC   AAY09371;
XX
DT   15-JUL-1999  (first entry)
XX
DE   Human apolipoprotein B17 protein sequence.
XX
KW   Human; apolipoprotein B17; apoB17; low density lipoprotein; LDL; heparin;
KW   blood vessel matrix; binding inhibition; atherosclerosis;
KW   apolipoprotein B.
XX
OS   Homo sapiens.
XX
PN   WO9918986-A1.
XX
PD   22-APR-1999.
XX
PF   09-OCT-1998;   98WO-US021345.
XX
PR   10-OCT-1997;   97US-0063468P.
PR   07-NOV-1997;   97US-00966296.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Goldberg IJ,  Pillarisetti S;
XX
DR   WPI; 1999-287883/24.
XX
PT   Inhibition of the binding of low density lipoprotein to blood vessel
PT   matrix.
XX
PS   Claim 3; Fig 1; 80pp; English.
XX
CC   The present invention describes a method for inhibiting the binding of
CC   low density lipoprotein (LDL) to blood vessel matrix in a subject. The
CC   method comprises administering to the subject a substance capable of
CC   binding to or competing with the amino-terminal region of apolipoprotein
CC   B (NTAB). Also described are: (a) a method of treating atherosclerosis;
CC   (b) identifying a compound capable of ameliorating atherosclerosis; (c) a
CC   compound identified by (b); (d) kits for inhibiting the binding of LDL to
CC   blood vessel matrix; and (e) and a mutant non-human organism that
CC   overproduces NTAB. The methods are useful for identifying compounds that
CC   inhibit binding of LDL to blood vessel matrix via the NTAB or compounds
CC   that compete with NTAB for binding to blood vessel matrix. These
CC   compounds, antibodies and B17 are useful for ameliorating
CC   atherosclerosis, the major cause of coronary heart disease and strokes.
CC   Competitive antagonists are useful in cases of overproduction of NTAB.
CC   The present sequence represents a specifically claimed NTAB designated
CC   apolipoprotein B17 or apoB17
XX
SQ   Sequence 809 AA;

  Query Match             100.0%;  Score 102;  DB 2;  Length 809;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 5
AAR06341
ID   AAR06341 standard; protein; 1671 AA.
XX
AC   AAR06341;
XX
DT   25-MAR-2003  (revised)
DT   14-DEC-1990  (first entry)
XX
DE   Signal peptide and first 1643 AAs of mature apoB protein.
XX
KW   Atherosclerosis; lipid binding peptide; LBP; phospholipid;
KW   Lecithin cholesterol acyl transferase; L-CAT; apo A1;
KW   Chinese hampster ovaries.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .27
FT                   /label= Signal peptide.
FT   Protein         28. .1671
FT                   /label= Mature peptide.
XX
PN   US4943527-A.
XX
PD   24-JUL-1990.
XX
PF   27-FEB-1986;   86US-00834300.
XX
PR   04-OCT-1985;   85US-00784418.
PR   04-DEC-1985;   85US-00804692.
XX
PA   (CALD ) CALIFORNIA BIOTECHNOLOGY INC.
XX
PI   Protter AA,  Vigne JL,  Mallory JB,  Talmadge KD,  Kane JP;
XX
DR   WPI; 1990-246622/32.
DR   N-PSDB; AAQ05590.
XX
PT   Prodn. of purified lipid-binding peptide - capable of binding to
PT   phospholipid(s), useful in e.g. atherosclerosis.
XX
PS   Disclosure; Page ?; -pp; English.
XX
CC   Lipid-binding peptides in conjunction with phospholipids are effective in
CC   reversing cholesterol transport, and may enhance lecithin cholesterol
CC   acetyl transferase, lowering the rate of plaque formation and
CC   atherosclerosis. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 1671 AA;

  Query Match             100.0%;  Score 102;  DB 2;  Length 1671;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 6
AAP70647
ID   AAP70647 standard; protein; 2721 AA.
XX
AC   AAP70647;
XX
DT   17-APR-1991  (first entry)
XX
DE   Sequence of N-terminal apolipoprotein B (apoB).
XX
KW   Lipid-binding peptide; apolipoprotein purification.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         87. .167
FT                   /label= Signal
FT   Protein         168. .8247
XX
PN   WO8702062-A.
XX
PD   09-APR-1987.
XX
PF   02-OCT-1986;   86WO-US002075.
XX
PR   04-OCT-1985;   85US-00784418.
```

PR 04-DEC-1985; 85US-00804692.
XX
PA (BIOT-) BIOTECHN RES PARTN.
XX
PI Protter AA, Vigne JL, Mallory JB, Talmadge KD;
XX
DR WPI; 1987-108703/15.
DR N-PSDB; AAN70996.
XX
PT Purified lipid-binding peptide prodn. - by expression of recombinant
PT system and adding lipid to obtd. peptide mixt. to form lipo-peptide
PT complex.
XX
PS Claim 50; pp73-85; 123pp; English.
XX
CC ApoB is a lipid-binding peptide adapted to bind to phospholipids at one
CC or more amphipatic alpha-helical peptide regions. ApoB gene is pref.
CC expressed in Chinese hamster ovary (CHO) cells and the gene is introduced
CC in an expression vector having a regulatable promoter derived from the
CC human metallothionein II gene
XX
SQ Sequence 2721 AA;

Query Match 100.0%; Score 102; DB 1; Length 2721;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEPTLEALFGK 20
||||||||||||||||||||
Db 688 IEIGLEGKGFEPTLEALFGK 707

RESULT 7
AAY31237
ID AAY31237 standard; protein; 3923 AA.
XX
AC AAY31237;
XX
DT 08-NOV-1999 (first entry)
XX
DE Human Apo B protein fragment.
XX
KW Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein;
KW Apo A1; low density lipoprotein; LDL; blood; therapy; atherosclerosis;
KW high density lipoprotein; HDL; cholesterol; coronary heart disease;
KW Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1. .3923
FT /label= Apo B
FT /note= "Partial sequence, no start codon given"
XX
PN WO9940789-A1.
XX
PD 19-AUG-1999.
XX
PF 28-AUG-1998; 98WO-US017908.
XX
PR 12-FEB-1998; 98US-0074497P.
PR 30-JUN-1998; 98US-00108006.
XX
PA (MINU) UNIV MINNESOTA.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI Steer CJ, Kren BT, Bandyopadhyay PT, Roy-Chowdhury J;
XX
DR WPI; 1999-527333/44.
DR N-PSDB; AAZ09525.
XX
PT Mutating apolipoprotein genes in hepatocytes to control cholesterol
PT levels, e.g. for treating or preventing hyperlipidemia, particularly
PT atherosclerosis.
XX
PS Claim 4; Page 75-83; 106pp; English.
XX
CC This invention describes a novel method for the genetic treatment of
CC hyperlipidemia by altering genes, in hepatocytes, for apoprotein (apo) B,
CC E or A1. Low density lipoprotein (LDL) levels in the blood are reduced by
CC altering an apo B gene (I) in a hepatocyte. The invention describes a
CC method for the therapeutic and/or prophylactic method involving altering
CC an apo E gene in hepatocytes by introducing the mutations Arg112Cys,
CC Arg158Cys or Cys158Arg and a method for ameliorating atherosclerosis by
CC altering the apo A1 gene in a hepatocyte so that the altered protein can
CC dimerize. Altering expression of apo genes regulates levels of high and
CC low density lipoprotein cholesterol. Altering expression of apo B, E and
CC A1 genes is used to treat or prevent atherosclerosis, coronary heart
CC disease, Alzheimer's disease, hypobetalipoproteinemia, and
CC dysbetalipoproteinemia. This sequence represents a fragment of the human
CC Apo B protein described in the method of the invention
XX
SQ Sequence 3923 AA;

Query Match 100.0%; Score 102; DB 2; Length 3923;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEPTLEALFGK 20
||||||||||||||||||||
Db 48 IEIGLEGKGFEPTLEALFGK 67

RESULT 8
AAW41262
ID AAW41262 standard; peptide; 4536 AA.
XX
AC AAW41262;
XX
DT 19-MAY-1998 (first entry)
XX
DE Apolipoprotein B-100.
XX
KW Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread;
KW thromboplastin-mediated process; cancer; inhibitor; blood coagulation;
KW angiogenesis; cellular differentiation; apoptosis; KRAD-14;
KW prothrombinase complex.
XX
OS Homo sapiens.
XX
PN WO9743311-A1.
XX
PD 20-NOV-1997.
XX
PF 09-MAY-1997; 97WO-GB001255.
XX
PR 09-MAY-1996; 96GB-00009702.
XX
PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI Bruckdorfer KR, Ettelaie C;
XX
DR WPI; 1998-008798/01.
XX
PT Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity -
PT used for treating or preventing coagulation, inhibiting angiogenesis,
PT cell differentiation and apoptosis.
XX
PS Disclosure; Page 42-47; 60pp; English.
XX
CC This sequence represents the human apoliporptoein B-100 (apoB-100).
CC Fragments of this sequence can be used in the peptide of the invention,
CC which has the formula (I), or their variants with one or more internal
CC deletions, insertions or substitutions, while retaining anti-coagulant
CC properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2
CC (I); X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-

```
CC   47 amino acids (aa); Z2 = the C terminus of the peptide, a terminal amide
CC   group or 1-77 aa. Compositions containing the peptide are used for
CC   simultaneous, separate or sequential treatment of cancer, particularly to
CC   prevent metastatic spread. They are also used to inhibit thromboplastin-
CC   mediated processes, specifically to prevent or reduce blood coagulation
CC   (e.g. during or after surgery or in cases of heart attack, stroke etc.)
CC   and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-
CC   14, which is active as such or as part of a 98-aa peptide, inhibits
CC   activation of the prothrombinase complex; and prevents activation of
CC   factor VII on the surface of thromboplastin and of platelets by thrombin.
CC   It binds to the residues 58-66 of thromboplastin. Since (I) are much
CC   smaller than apoB-100, they act more quickly
XX
SQ   Sequence 4536 AA;

  Query Match             100.0%;  Score 102;  DB 2;  Length 4536;
  Best Local Similarity   100.0%;  Pred. No. 4e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        661 IEIGLEGKGFEPTLEALFGK 680


RESULT 9
AAW96826
ID   AAW96826 standard; protein; 4536 AA.
XX
AC   AAW96826;
XX
DT   22-APR-1999  (first entry)
XX
DE   Amino acid sequence of human apolipoprotein B-100 (apoB-100).
XX
KW   Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;
KW   apolipoprotein; binding; in vivo transport; nucleic acid; binding domain;
KW   nuclear localisation sequence; gene therapy; cancer; cystic fibrosis;
KW   non-small cell lung carcinoma; diabetes; arteriosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO9856938-A1.
XX
PD   17-DEC-1998.
XX
PF   10-JUN-1998;   98WO-US011927.
XX
PR   13-JUN-1997;   97US-00874807.
PR   14-MAY-1998;   98US-00079030.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Guevara JG,  Hoogeveen RC,  Moore JP;
XX
DR   WPI; 1999-070331/06.
XX
PT   Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
PT   used for delivering nucleic acid to cells for gene therapy and antisense
PT   treatment.
XX
PS   Disclosure; Fig 1A-C; 293pp; English.
XX
CC   The present sequence represents human apolipoprotein B-100 (apoB-100).
CC   ApoB-100 is a major apoprotein component of very-low density lipoproteins
CC   (VLDL), intermediate density lipoprotein (IDL), low density lipoproteins
CC   ((LDL) and lipoprotein a. The specification describes a composition that
CC   comprises LDL and apolipoproteins for the binding and in vivo transport
CC   of nucleic acids. Binding domains (see AAW96827-77) and nuclear
CC   localisation sequences (see AAW96878-97) for use in the composition can
CC   be derived from the present sequence. The composition is used to deliver
CC   nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a
CC   therapeutic polypeptide or antisense molecule (or ribozyme). Specifically
CC   they are used for gene therapy of cancers (particularly non-small cell
CC   lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
XX
SQ   Sequence 4536 AA;

  Query Match             100.0%;  Score 102;  DB 2;  Length 4536;
  Best Local Similarity   100.0%;  Pred. No. 4e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        661 IEIGLEGKGFEPTLEALFGK 680


RESULT 10
AAU98981
ID   AAU98981 standard; protein; 4560 AA.
XX
AC   AAU98981;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human apolipoprotein B100 (apoB100).
XX
KW   Human; low density lipoprotein receptor; LDLR; apolipoprotein E; apoE;
KW   virus-lipoprotein complex; apolipoprotein B100; apoB100; VSV;
KW   Flaviviridae virus; vesicular stomatitis virus; cholesterol metabolism.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          2835. .4189
FT                   /note= "Epitope region; specifically claimed in claim 11"
FT   Region          2980. .3084
FT                   /note= "Epitope region; specifically claimed in claim 11"
XX
PN   WO200248388-A2.
XX
PD   20-JUN-2002.
XX
PF   24-OCT-2001; 2001WO-US050701.
XX
PR   25-OCT-2000; 2000US-0243594P.
XX
PA   (AGNE/) AGNELLO V.
XX
PI   Agnello V;
XX
DR   WPI; 2002-583528/62.
XX
PT   Inhibiting infection of cell by virus capable of forming complex with
PT   lipoprotein, by preventing formation or altering conformation of complex,
PT   or blocking cell receptor for the complex using antibody to receptor.
XX
PS   Claim 11; Page 44-47; 49pp; English.
XX
CC   The invention relates to a method of inhibiting infection of a cell by
CC   virus capable of forming a complex with lipoprotein. The method comprises
CC   preventing formation of and altering conformation of the complex to
CC   prevent its interaction with cell receptor (CR), blocking CR using
CC   antibody to receptor or binding of lipoprotein complex to CR using
CC   soluble lipoprotein receptor, or downregulating low density lipoprotein
CC   receptor activity of cells. In this method, inhibition of infection
CC   involves preventing formation of a complex between the lipoprotein and
CC   virus, and dissociating the virus and lipoprotein, or by introducing
CC   lipase to the cell, which is capable of inducing a conformational change
CC   of a virus-lipoprotein complex. Alternatively, the method involves
CC   introducing anti-low density lipoprotein (LDL) receptor antibody (anti-
CC   LDLR) which binds to an epitope included in the ligand binding domain of
CC   LDL receptor, or anti-apolipoprotein (apo)B100 antibody which binds to an
CC   epitope included in the LDL-receptor binding domain of apoB100, or anti-
CC   apoE antibody which binds to an epitope included in LDL receptor binding
CC   domain of apoE. The method also involves introducing a peptide comprising
CC   the soluble 5th repeat of the ligand binding domain of LDL receptor,
```

```
CC   where the peptide fragment binds to the receptor binding domain of apoB
CC   or apoE; or downregulating lipoprotein receptor activity of the receptor.
CC   The method is useful for inhibiting or preventing infection of a cell by
CC   viruses such as Flaviviridae virus, vesicular stomatitis virus or other
CC   viruses that complex with LDL or very low-density lipoprotein (VLDL). The
CC   inhibition of infection occurs without harmful effects on cholesterol
CC   metabolism. The present sequence represents apolipoprotein B100 (apoB100)
XX
SQ   Sequence 4560 AA;

  Query Match             100.0%;  Score 102;  DB 5;  Length 4560;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        685 IEIGLEGKGFEPTLEALFGK 704


RESULT 11
ADD48677
ID   ADD48677 standard; protein; 4561 AA.
XX
AC   ADD48677;
XX
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein X04714, SEQ ID NO 14384.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; X04714.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 4561 AA;

  Query Match             100.0%;  Score 102;  DB 7;  Length 4561;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        685 IEIGLEGKGFEPTLEALFGK 704


RESULT 12
AAO15893
ID   AAO15893 standard; protein; 4563 AA.
XX
AC   AAO15893;
XX
DT   30-JAN-2003  (first entry)
XX
DE   Human apolipoprotein B (APOB).
XX
KW   Human; gene therapy; single nucleotide polymorphism; SNP;
KW   cytochrome C oxidase subunit VIb; COX6B; high serum cholesterol; GPI-1;
KW   N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
KW   glycosylphosphatidylinositol-1; low serum high density lipoprotein.
XX
OS   Homo sapiens.
XX
PN   WO200272604-A2.
XX
PD   19-SEP-2002.
XX
PF   05-MAR-2002; 2002WO-US006728.
XX
PR   09-MAR-2001; 2001US-00802640.
XX
PA   (SEQU-) SEQUENOM INC.
XX
PI   Braun A,  Bansal A,  Kleyn PW;
XX
DR   WPI; 2002-750478/81.
DR   N-PSDB; ABT13015.
XX
PT   Detecting the presence or absence of an allelic variant of a polymorphic
PT   region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
PT   to high serum cholesterol, low serum HDL and cardiovascular disease.
XX
PS   Disclosure; Page 158-168; 199pp; English.
XX
CC   The invention comprises methods of detecting the presence or absence of
CC   at least one allelic variant of a polymorphic region of a gene associated
CC   with cardiovascular disease. The invention specifically relates to
CC   detecting the region of a cytochrome C oxidase subunit VIb (COX6B) gene
CC   that is associated with high serum cholesterol, or the region of the N-
CC   acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
CC   (GPI-1) gene that is associated with low serum high density lipoprotein
CC   (HDL). The methods of the invention are useful for detecting a
CC   predisposition to high serum cholesterol, low serum HDL and
```

```
CC   cardiovascular disease. The methods are also useful for elucidating
CC   pathological pathways, developing diagnostic assays and new drug
CC   therapies for such disorders. The present amino acid sequence represents
CC   a human protein that is associated with high serum cholesterol, low serum
CC   HDL and/or cardiovascular disease
XX
SQ   Sequence 4563 AA;

  Query Match             100.0%;  Score 102;  DB 5;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 13
ABR40253
ID   ABR40253 standard; protein; 4563 AA.
XX
AC   ABR40253;
XX
DT   20-JUN-2003  (first entry)
XX
DE   Human alipoprotein B.
XX
KW   Human; alipoprotein B; ApoB; antilipaemic; antiarteriosclerotic;
KW   antidiabetic; anorectic; cardiovascular; gene therapy; lipid metabolism;
KW   cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes;
KW   type 2 diabetes; obesity; atherosclerosis; cardiovascular disease;
KW   glucose.
XX
OS   Homo sapiens.
XX
PN   WO2003011887-A2.
XX
PD   13-FEB-2003.
XX
PF   30-JUL-2002; 2002WO-US024247.
XX
PR   01-AUG-2001; 2001US-00920033.
PR   30-APR-2002; 2002US-00135985.
PR   15-MAY-2002; 2002US-00147196.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Crooke RM,  Graham MJ;
XX
DR   WPI; 2003-268105/26.
DR   N-PSDB; ACC62114.
XX
PT   New antisense oligonucleotides for modulating apolipoprotein B,
PT   especially for preventing or treating atherosclerosis, hyperlipidemia or
PT   diabetes, or for modulating glucose, cholesterol, lipoprotein or
PT   triglyceride levels.
XX
PS   Disclosure; Page 118-138; 160pp; English.
XX
CC   The invention relates to a novel compound that is 8-50 nucleotides in
CC   length that is targeted to a nucleic acid molecule encoding
CC   apolipoprotein B (ApoB), and specifically hybridises with and inhibits
CC   the expression of a nucleic acid molecule encoding ApoB; or which
CC   specifically hybridises with at least an 8-nucleotide portion of an
CC   active site on a nucleic acid molecule encoding ApoB. A compound of the
CC   invention has antilipaemic, antiarteriosclerotic, antidiabetic,
CC   anorectic, and cardiovascular activity. The compound may have a use in
CC   gene therapy. The antisense oligonucleotide is useful for treating an
CC   animal having a disease or conditions associated with ApoB, e.g. a
CC   condition involving abnormal lipid metabolism, a condition involving
CC   abnormal cholesterol metabolism, atherosclerosis, or a condition
CC   involving an abnormal metabolic condition (e.g. hyperlipidaemia, diabetes
CC   (specifically Type 2 diabetes), obesity, atherosclerosis or
CC   cardiovascular disease). The new compound or the antisense
CC   oligonucleotide is also useful for modulating glucose levels
CC   (particularly plasma or serum glucose levels) in a human or diabetic
CC   animal, or for modulating serum cholesterol levels, lipoprotein levels
CC   (specifically VLDL, HDL or LDL) or serum triglyceride levels,
CC   particularly in a human. The antisense compound is also useful for
CC   preventing or delaying the onset of a disease or condition associated
CC   with ApoB, or the onset of an increase in glucose levels in the animal or
CC   human. The present sequence is used in the exemplification of the
CC   invention
XX
SQ   Sequence 4563 AA;

  Query Match             100.0%;  Score 102;  DB 6;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 14
ABU79140
ID   ABU79140 standard; protein; 4563 AA.
XX
AC   ABU79140;
XX
DT   18-JUN-2003  (first entry)
XX
DE   Apolipoprotein #2.
XX
KW   Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW   gene therapy; mammalian cell receptor; cytostatic;
KW   tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
KW   tumouricidal immunocyte; antitumour.
XX
OS   Unidentified.
XX
PN   US2002177551-A1.
XX
PD   28-NOV-2002.
XX
PF   30-MAY-2001; 2001US-00870759.
XX
PR   31-MAY-2000; 2000US-0208128P.
XX
PA   (TERM/) TERMAN D S.
XX
PI   Terman DS;
XX
DR   WPI; 2003-361759/34.
DR   N-PSDB; ACA64742.
XX
PT   A mammalian cell receptor, useful in the treatment of cancer by binding
PT   to tumor associated lipids where the binding induces anergy or apoptosis
PT   in T cells and antigen presenting cells.
XX
PS   Example 2; Page; 167pp; English.
XX
CC   The invention relates to a mammalian cell receptor, useful in the
CC   treatment of cancer, which binds to tumour associated lipids and induces
CC   anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC   Also included are a mammalian cell useful in the treatment of cancer
CC   where the receptor which binds tumour associated lipids and induces
CC   cellular inactivation or death is deleted or functionally deactivated,
CC   producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC   (by allowing tumour associated lipids to contact immunocytes in which
CC   receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC   sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC   sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC   deleted), a construct useful in the treatment of cancer comprising a
CC   superantigen (SAg) nucleotide inserted into a virus, a mammalian T cell
```

```
CC   useful in the treatment of cancer (where an adaptor protein which
CC   inhibits T cell activation by tumour associated antigens is deleted or
CC   functionally deactivated), a composition useful in the treatment of
CC   cancer (comprising a lipid raft conjugated to a superantigen), producing
CC   (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC   allowing tumour associated lipids to contact immunocytes, in which
CC   receptors for the lipids are inactivated or deleted to produce a
CC   tumouricidal immunocyte population, and administering the tumouricidally
CC   activated immunocytes to the host), producing (M3) a tumouricidal APC
CC   population ex vivo in a mammal (by allowing a tumour associated lipid to
CC   contact APCs, in which receptors for the tumour associated lipids are
CC   inactivated or deleted to produce a tumouricidally activated population,
CC   and administering APCs to the host), producing a tumouricidal T cell
CC   population ex vivo in a mammal) by allowing a tumour associated lipids to
CC   contact T cells, in which adaptor proteins, which inhibit T cell
CC   activation by tumour associated antigens, are deleted or functionally
CC   deactivated to produce a tumouricidal population of T cells, and
CC   administering the tumouricidally activated T cells to the host, or
CC   allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC   administering the tumouricidally activated T cells to the host), treating
CC   (M5) cancer in a mammal (by administering a lipid binding molecule which
CC   binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC   a tumouricidal T cell population in vivo in a mammal (by allowing a
CC   tumour associated antigen to contact immunocytes in which adaptor
CC   proteins which inhibit T cell activation by tumour associated antigens
CC   are deleted or functionally deactivated) and producing (M7) a
CC   tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC   superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC   receptors, methods and compositions are useful for treating cancers and
CC   tumours. Bacterial superantigens are co-administered or administered as
CC   fusion constructs with anti-tumour proteins or motifs. The present
CC   sequence represents an anti-tumour protein which is co-administered with
CC   or incorporated into a fusion construct with a superantigen. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format from the US patnet
CC   office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ   Sequence 4563 AA;

  Query Match             100.0%;  Score 102;  DB 6;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 15
ADF43408
ID   ADF43408 standard; protein; 4563 AA.
XX
AC   ADF43408;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Apolipoprotein polypeptide seqid 128.
XX
KW   receptor; lipid-based tumour associated antigen; cytostatic;
KW   antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW   infectious disease; apolipoprotein.
XX
OS   Unidentified.
XX
PN   US2003157113-A1.
XX
PD   21-AUG-2003.
XX
PF   28-DEC-2000; 2000US-00751708.
XX
PR   28-DEC-1999;   99US-0173371P.
XX
PA   (TERM/) TERMAN D S.
XX
PI   Terman DS;
XX
DR   WPI; 2003-787326/74.
DR   N-PSDB; ADF43407.
XX
PT   New receptor in a mammalian cell that inhibits regular activation by
PT   receptors specific for lipid-based tumor associated antigens, useful for
PT   treating a neoplastic disease or tumor, and infectious diseases.
XX
PS   Example 3; SEQ ID NO 128; 151pp; English.
XX
CC   The invention describes a receptor in a mammalian cell that inhibits
CC   regular activation by receptors specific for lipid-based tumour
CC   associated antigen. The receptor has cytostatic and antimicrobial
CC   properties and is suitable for use in gene therapy. The receptors,
CC   methods and compositions are useful for treating a neoplastic disease or
CC   tumour (cancer), and infectious diseases. This sequence represents
CC   apolipoprotein polypeptide, a cell surface moiety, the DNA of which can
CC   be transfected into a cell with superantigen DNA to generate antitumour
CC   immunity.
XX
SQ   Sequence 4563 AA;

  Query Match             100.0%;  Score 102;  DB 7;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


Search completed: March 21, 2006, 18:52:10
Job time : 191 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 18:56:28 ; Search time 47 Seconds
(without alignments)
35.181 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	50	2	US-09-079-030-13	Sequence 13, Appl
2	102	100.0	4536	2	US-09-180-422B-27	Sequence 27, Appl
3	102	100.0	4536	2	US-09-079-030-1	Sequence 1, Appli
4	102	100.0	4563	2	US-09-108-006C-1	Sequence 1, Appli
5	102	100.0	4563	2	US-09-538-092-842	Sequence 842, App
6	48	47.1	383	2	US-09-902-540-16490	Sequence 16490, A
7	47	46.1	263	2	US-09-489-039A-12585	Sequence 12585, A
8	46	45.1	458	2	US-09-583-110-5167	Sequence 5167, Ap
9	46	45.1	463	2	US-09-107-433-3506	Sequence 3506, Ap
10	44	43.1	203	2	US-09-252-991A-17282	Sequence 17282, A
11	44	43.1	986	2	US-08-872-757-4	Sequence 4, Appli
12	44	43.1	986	2	US-09-850-048A-4	Sequence 4, Appli
13	43	42.2	149	2	US-09-489-039A-9379	Sequence 9379, Ap
14	43	42.2	530	2	US-09-107-433-5169	Sequence 5169, Ap
15	43	42.2	655	2	US-09-583-110-2958	Sequence 2958, Ap
16	43	42.2	1160	2	US-09-328-352-6457	Sequence 6457, Ap
17	43	42.2	1516	2	US-09-949-016-8209	Sequence 8209, Ap
18	42	41.2	85	2	US-09-198-452A-1281	Sequence 1281, Ap
19	42	41.2	306	2	US-09-107-532A-6274	Sequence 6274, Ap
20	42	41.2	307	2	US-09-902-540-10923	Sequence 10923, A
21	41.5	40.7	370	2	US-09-489-039A-9818	Sequence 9818, Ap
22	41.5	40.7	431	2	US-09-900-237-28	Sequence 28, Appl
23	41.5	40.7	506	2	US-09-900-237-20	Sequence 20, Appl
24	41.5	40.7	701	2	US-09-900-237-32	Sequence 32, Appl
25	41.5	40.7	881	2	US-08-960-048-8	Sequence 8, Appli
26	41.5	40.7	881	2	US-09-838-586-8	Sequence 8, Appli
27	41.5	40.7	1043	2	US-10-160-719A-50	Sequence 50, Appl
28	41.5	40.7	1065	2	US-09-221-013A-10	Sequence 10, Appl
29	41.5	40.7	1065	2	US-09-900-237-33	Sequence 33, Appl
30	41.5	40.7	1077	2	US-10-160-719A-6	Sequence 6, Appli
31	41.5	40.7	1077	2	US-10-160-719A-30	Sequence 30, Appl
32	41.5	40.7	1077	2	US-10-209-059-10	Sequence 10, Appl
33	41.5	40.7	1079	2	US-10-209-059-22	Sequence 22, Appl
34	41.5	40.7	1080	2	US-09-900-237-30	Sequence 30, Appl
35	41	40.2	107	2	US-09-107-532A-6669	Sequence 6669, Ap
36	41	40.2	137	2	US-09-710-279-1980	Sequence 1980, Ap
37	41	40.2	213	2	US-09-413-814-26	Sequence 26, Appl
38	41	40.2	267	1	US-08-557-128-4	Sequence 4, Appli
39	41	40.2	267	2	US-09-242-690A-36	Sequence 36, Appl
40	41	40.2	267	2	US-09-908-855-36	Sequence 36, Appl
41	41	40.2	315	2	US-09-543-681A-7048	Sequence 7048, Ap
42	41	40.2	367	2	US-09-134-001C-5557	Sequence 5557, Ap
43	41	40.2	401	2	US-09-252-991A-29704	Sequence 29704, A
44	41	40.2	478	2	US-09-107-532A-4922	Sequence 4922, Ap
45	41	40.2	517	2	US-09-902-540-10229	Sequence 10229, A

ALIGNMENTS

RESULT 1
US-09-079-030-13
; Sequence 13, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogeveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: ARAG:003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-13

6,635,623

Query Match 100.0%; Score 102; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEPTLEALFGK 20
||||||||||||||||||||
Db 10 IEIGLEGKGFEPTLEALFGK 29

```
RESULT 2
US-09-180-422B-27
; Sequence 27, Application US/09180422B
; Patent No. 6444644
;  GENERAL INFORMATION:
;       APPLICANT: BRUCKDORFER, KARL R
;                  ETTELAIE, CAMILLE
;       TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
;                           FROM APOLIPOPROTEIN B-100
;       NUMBER OF SEQUENCES: 27
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: NIXON & VANDERHYE, P.C.
;            STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
;            CITY: ARLINGTON
;            STATE: VA
;            COUNTRY: USA
;            ZIP: 22201
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/180,422B
;            FILING DATE: 07-Dec-1998
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SADOFF, B.J.
;            REGISTRATION NUMBER: 36663
;            REFERENCE/DOCKET NUMBER: 117-268
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 7038164000
;            TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 27:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 4536 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27

  Query Match             100.0%;  Score 102;  DB 2;  Length 4536;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        661 IEIGLEGKGFEPTLEALFGK 680


RESULT 3
US-09-079-030-1
; Sequence 1, Application US/09079030
; Patent No. 6635623
;  GENERAL INFORMATION:
;    APPLICANT:  Guevera, Jr., Juan G.
;    APPLICANT:  Hoogeveen, Ron C.
;    APPLICANT:  Moore, Paul J.
;    TITLE OF INVENTION:  LIPOPROTEINS AS NUCLEIC ACID DELIVERY
;    TITLE OF INVENTION:  VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
;    NUMBER OF SEQUENCES:  229
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Arnold, White & Durkee
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,030
;      FILING DATE:  Concurrently Herewith
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMillian, Nabeela R.
;      REGISTRATION NUMBER:  P-43,363
;      REFERENCE/DOCKET NUMBER:  ARAG:003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512/418-3000
;      TELEFAX:  512/474-7577
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4536 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-09-079-030-1

  Query Match             100.0%;  Score 102;  DB 2;  Length 4536;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        661 IEIGLEGKGFEPTLEALFGK 680


RESULT 4
US-09-108-006C-1
; Sequence 1, Application US/09108006C
; Patent No. 6524613
;  GENERAL INFORMATION:
;       APPLICANT: Steer, Clifford J.
;                  Kren, Betsy T.
;                  Bandyopadhyay, Paramita
;                  Roy-Chowdhury, Jayanta
;       TITLE OF INVENTION: Hepatocellular Chimeraplasty
;       NUMBER OF SEQUENCES: 62
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Kimeragen, Inc.
;            STREET: 300 Pheasant Run
;            CITY: Newtown
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 18940
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/108,006C
;            FILING DATE: 30-Jun-1992
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/054,288
;            FILING DATE: 30-APR-1997
;            APPLICATION NUMBER: 60/054,837
;            FILING DATE: 05-AUG-1997
;            APPLICATION NUMBER: 60/064,996
;            FILING DATE: 10-NOV-1997
;            APPLICATION NUMBER: 60/074,497
;            FILING DATE: 12-FEB-1998
;            APPLICATION NUMBER: PCT US 98/08834
;            FILING DATE: 30-APR-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Friebel, Thomas
;            REGISTRATION NUMBER: 29258
;            REFERENCE/DOCKET NUMBER: 7991-015-999
```

```
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 215-504-4444
;              TELEFAX: 215-504-4545
;              TELEX: <Unknown>
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 4563 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-108-006C-1

  Query Match             100.0%;  Score 102;  DB 2;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 5
US-09-538-092-842
; Sequence 842, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 842
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P04114
US-09-538-092-842

  Query Match             100.0%;  Score 102;  DB 2;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 6
US-09-902-540-16490
; Sequence 16490, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16490
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-16490

  Query Match             47.1%;  Score 48;  DB 2;  Length 383;
  Best Local Similarity   66.7%;  Pred. No. 8.5;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GLEGKGFEPTLEALF 18
              ||:||||   |:|||
Db         62 GLKGKGFLSLLKALF 76


RESULT 7
US-09-489-039A-12585
; Sequence 12585, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 12585
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12585

  Query Match             46.1%;  Score 47;  DB 2;  Length 263;
  Best Local Similarity   55.6%;  Pred. No. 8;
  Matches   10;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFEPTLEALFGK 20
              |  :|   :|||||| ||
Db        120 IAAKGSPIQPTLEALKGK 137


RESULT 8
US-09-583-110-5167
; Sequence 5167, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
;  APPLICANT:  Lynn Doucette-Stamm et al.
;  TITLE OF INVENTION:  Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE:  PATH00-07A
;  CURRENT APPLICATION NUMBER: US/09/583,110
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 09/107,433
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/085,131
;  PRIOR FILING DATE:  1998-05-12
;  PRIOR APPLICATION NUMBER:  US 60/051,553
;  PRIOR FILING DATE:  1997-07-02
;  NUMBER OF SEQ ID NOS:  5322
; SEQ ID NO 5167
;   LENGTH: 458
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-5167

  Query Match             45.1%;  Score 46;  DB 2;  Length 458;
  Best Local Similarity   61.1%;  Pred. No. 23;
  Matches   11;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;
```

```
Qy          2 EIGLEGKGFEPTLEALFG 19
              ||||||| ||  :  ||
Db        136 EIGLEGKLSEPEGQRNFG 153

RESULT 9
US-09-107-433-3506
; Sequence 3506, Application US/09107433
; Patent No. 6800744
;  GENERAL INFORMATION:
;       APPLICANT: Lynn A Doucette-Stamm  and David Bush
;       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                           SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNO
;                           THERAPEUTICS
;       NUMBER OF SEQUENCES: 5206
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;            STREET: 100 Beaver Street
;            CITY: Waltham
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02354
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: CD/ROM ISO9660
;            COMPUTER: <Unknown>
;            OPERATING SYSTEM: <Unknown>
;            SOFTWARE: <Unknown>
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/107,433
;            FILING DATE: 30-Jun-1998
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/ 085131
;            FILING DATE: May 12, 1998
;            APPLICATION NUMBER: 60/051553
;            FILING DATE: July 2, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ariniello, Pamela Deneke
;            REGISTRATION NUMBER: 40,489
;            REFERENCE/DOCKET NUMBER: GTC-011
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (781)893-5007
;            TELEFAX: (781)893-8277
;  INFORMATION FOR SEQ ID NO: 3506:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 463 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       HYPOTHETICAL: YES
;       ORIGINAL SOURCE:
;            ORGANISM: Streptococcus pneumoniae
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION: (B) LOCATION 1...463
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3506:
US-09-107-433-3506

  Query Match             45.1%;  Score 46;  DB 2;  Length 463;
  Best Local Similarity   61.1%;  Pred. No. 23;
  Matches   11;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFG 19
              ||||||| ||  :  ||
Db        141 EIGLEGKLSEPEGQRNFG 158


RESULT 10
US-09-252-991A-17282
; Sequence 17282, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 17282
;   LENGTH: 203
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17282

  Query Match             43.1%;  Score 44;  DB 2;  Length 203;
  Best Local Similarity   57.1%;  Pred. No. 19;
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 LEGKGFEPTLEALF 18
              | |:||:| |:|:|
Db        107 LGGEGFQPYLKAVF 120


RESULT 11
US-08-872-757-4
; Sequence 4, Application US/08872757
; Patent No. 6258584
;  GENERAL INFORMATION:
;    APPLICANT:  Prockop, Darwin J.
;    APPLICANT:  Hojima, Yoshio
;    APPLICANT:  Li, Shi-Wu
;    APPLICANT:  Sieron, Aleksander
;    TITLE OF INVENTION:  RECOMBINANT C-PROTEINASE AND
;    TITLE OF INVENTION:  PROCESSES; METHODS AND USES THEREOF
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/872,757
;      FILING DATE:  10-JUN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,187
;      FILING DATE:  01-MAR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  8389-028-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  986 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-872-757-4

  Query Match             43.1%;  Score 44;  DB 2;  Length 986;
```

```
  Best Local Similarity   61.5%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 GKGFEPTLEALFG 19
              |||| |  ||::|
Db        424 GKGFFPVYEAMWG 436


RESULT 12
US-09-850-048A-4
; Sequence 4, Application US/09850048A
; Patent No. 6562613
;   GENERAL INFORMATION:
;        APPLICANT: Prockop, Darwin J.
;                   Hojima, Yoshio
;                   Li, Shi-Wu
;                   Sieron, Aleksander
;        TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
;                            PROCESSES; METHODS AND USES THEREOF
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: New York
;             COUNTRY: U.S.A.
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/850,048A
;             FILING DATE: 07-May-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/609,187
;             FILING DATE: 1996-03-01
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Halluin, Albert P.
;             REGISTRATION NUMBER: 25,227
;             REFERENCE/DOCKET NUMBER: 8389-028-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-854-3660
;             TELEFAX: 415-854-3694
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 986 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-850-048A-4

  Query Match             43.1%;  Score 44;  DB 2;  Length 986;
  Best Local Similarity   61.5%;  Pred. No. 1.2e+02;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 GKGFEPTLEALFG 19
              |||| |  ||::|
Db        424 GKGFFPVYEAMWG 436


RESULT 13
US-09-489-039A-9379
; Sequence 9379, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 9379
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9379

  Query Match             42.2%;  Score 43;  DB 2;  Length 149;
  Best Local Similarity   35.0%;  Pred. No. 19;
  Matches    7;  Conservative    5;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              :|||::  | :  |   ||:
Db          6 VEIGIDAPGIDALLRRTFGR 25


RESULT 14
US-09-107-433-5169
; Sequence 5169, Application US/09107433
; Patent No. 6800744
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;                            SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE   FOR DIAGNC
;                            THERAPEUTICS
;        NUMBER OF SEQUENCES: 5206
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: <Unknown>
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,433
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/ 085131
;             FILING DATE: May 12, 1998
;             APPLICATION NUMBER: 60/051553
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-011
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 5169:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 530 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        HYPOTHETICAL: YES
;        ORIGINAL SOURCE:
;             ORGANISM: Streptococcus pneumoniae
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...530
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5169:
US-09-107-433-5169
```

```
  Query Match             42.2%;  Score 43;  DB 2;  Length 530;
  Best Local Similarity   77.8%;  Pred. No. 85;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFE 11
              :||:|||||
Db        456 VGLDGKGFE 464


RESULT 15
US-09-583-110-2958
; Sequence 2958, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
;  APPLICANT:  Lynn Doucette-Stamm et al.
;  TITLE OF INVENTION:  Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;  TITLE OF INVENTION:  Pneumoniae for Diagnostics and Therapeutics
;  FILE REFERENCE:  PATH00-07A
;  CURRENT APPLICATION NUMBER: US/09/583,110
;  CURRENT FILING DATE:  2000-05-26
;  PRIOR APPLICATION NUMBER:  US 09/107,433
;  PRIOR FILING DATE:  1998-06-30
;  PRIOR APPLICATION NUMBER:  US 60/085,131
;  PRIOR FILING DATE:  1998-05-12
;  PRIOR APPLICATION NUMBER:  US 60/051,553
;  PRIOR FILING DATE:  1997-07-02
;  NUMBER OF SEQ ID NOS:  5322
; SEQ ID NO 2958
;   LENGTH: 655
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-2958

  Query Match             42.2%;  Score 43;  DB 2;  Length 655;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFE 11
              :||:|||||
Db        581 VGLDGKGFE 589


Search completed: March 21, 2006, 18:57:45
Job time : 48 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:07:38 ; Search time 165 Seconds
(without alignments)
50.646 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	20	4	US-10-115-072-32	Sequence 32, Appl
2	102	100.0	20	4	US-10-679-032-70	Sequence 70, Appl
3	102	100.0	50	5	US-10-656-053B-13	Sequence 13, Appl
4	102	100.0	4536	5	US-10-656-053B-1	Sequence 1, Appli
5	102	100.0	4560	5	US-10-398-200-2	Sequence 2, Appli
6	102	100.0	4563	3	US-09-870-759-128	Sequence 128, App
7	102	100.0	4563	3	US-09-802-640-32	Sequence 32, Appl
8	102	100.0	4563	3	US-09-751-708A-128	Sequence 128, App
9	102	100.0	4563	4	US-10-403-902A-32	Sequence 32, Appl
10	102	100.0	4563	4	US-10-741-601-432	Sequence 432, App
11	102	100.0	4563	4	US-10-741-601-433	Sequence 433, App
12	102	100.0	4563	4	US-10-428-817A-124	Sequence 124, App
13	102	100.0	4563	5	US-10-741-600-1287	Sequence 1287, Ap
14	102	100.0	4563	5	US-10-741-600-1288	Sequence 1288, Ap
15	102	100.0	4563	5	US-10-868-577A-25	Sequence 25, Appl
16	102	100.0	4563	5	US-10-937-758A-105	Sequence 105, App
17	80	78.4	210	5	US-10-808-052A-13	Sequence 13, Appl
18	80	78.4	210	6	US-11-054-931-19	Sequence 19, Appl
19	48	47.1	73	4	US-10-437-963-142631	Sequence 142631,
20	47.5	46.6	445	4	US-10-108-260A-3729	Sequence 3729, Ap
21	47.5	46.6	445	5	US-10-741-600-1464	Sequence 1464, Ap
22	47	46.1	91	4	US-10-767-701-37316	Sequence 37316, A
23	47	46.1	275	4	US-10-437-963-114424	Sequence 114424,
24	47	46.1	403	4	US-10-100-294A-33	Sequence 33, Appl
25	47	46.1	403	4	US-10-100-294A-42	Sequence 42, Appl
26	47	46.1	431	4	US-10-286-264-38	Sequence 38, Appl
27	47	46.1	431	4	US-10-225-068-192	Sequence 192, App
28	47	46.1	431	4	US-10-374-780A-42	Sequence 42, Appl
29	47	46.1	431	4	US-10-412-699B-172	Sequence 172, App
30	47	46.1	431	5	US-10-225-068-192	Sequence 192, App
31	46.5	45.6	154	4	US-10-425-114-58038	Sequence 58038, A
32	46	45.1	326	4	US-10-369-493-18294	Sequence 18294, A
33	46	45.1	351	4	US-10-424-599-276962	Sequence 276962,
34	46	45.1	437	4	US-10-282-122A-50313	Sequence 50313, A
35	46	45.1	463	5	US-10-617-320-3506	Sequence 3506, Ap
36	46	45.1	502	4	US-10-474-776-295	Sequence 295, App
37	46	45.1	502	5	US-10-472-928-1880	Sequence 1880, Ap
38	45	44.1	89	4	US-10-437-963-121126	Sequence 121126,
39	45	44.1	440	4	US-10-369-493-18601	Sequence 18601, A
40	45	44.1	459	4	US-10-425-114-40565	Sequence 40565, A
41	45	44.1	492	4	US-10-437-963-111267	Sequence 111267,
42	44	43.1	289	3	US-09-815-242-10747	Sequence 10747, A
43	44	43.1	289	4	US-10-282-122A-42585	Sequence 42585, A
44	44	43.1	289	5	US-10-953-901-320	Sequence 320, App
45	44	43.1	289	5	US-10-953-901-322	Sequence 322, App

ALIGNMENTS

RESULT 1
US-10-115-072-32
; Sequence 32, Application US/10115072
; Publication No. US20030105003A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF
; TITLE OF INVENTION: ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY
; TITLE OF INVENTION: FOR DETERMINATION OF IMMUNE RESPONSES AGAINST OXIDIZED
; TITLE OF INVENTION: LOW DENSITY LIPOPROTEIN
; FILE REFERENCE: 03940.0057
; CURRENT APPLICATION NUMBER: US/10/115,072
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/281,410
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0101232-7
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0103754-8
; PRIOR FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-115-072-32

Query Match 100.0%; Score 102; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEPTLEALFGK 20
||||||||||||||||||||
Db 1 IEIGLEGKGFEPTLEALFGK 20

RESULT 2
US-10-679-032-70
; Sequence 70, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR

```
;  TITLE OF INVENTION:  TREATMENT OF ATHEROSCLEROSIS
;  FILE REFERENCE: 7303CIP
;  CURRENT APPLICATION NUMBER: US/10/679,032
;  CURRENT FILING DATE:  2003-10-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-679-032-70

  Query Match            100.0%;  Score 102;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 3
US-10-656-053B-13
; Sequence 13, Application US/10656053B
; Publication No. US20050215499A1
; GENERAL INFORMATION:
;  APPLICANT: GUEVERA, JR., JUAN G.
;  APPLICANT:  HOOGEVEEN, RON C.
;  APPLICANT:  MOORE, PAUL J.
;  TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID VECTORS
;  FILE REFERENCE: ARAG:003USD1
;  CURRENT APPLICATION NUMBER: US/10/656,053B
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: 09/079,030
;  PRIOR FILING DATE: 1998-05-14
;  PRIOR APPLICATION NUMBER: 08/874,807
;  PRIOR FILING DATE: 1997-06-13
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 50
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-053B-13

  Query Match            100.0%;  Score 102;  DB 5;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db         10 IEIGLEGKGFEPTLEALFGK 29


RESULT 4
US-10-656-053B-1
; Sequence 1, Application US/10656053B
; Publication No. US20050215499A1
; GENERAL INFORMATION:
;  APPLICANT: GUEVERA, JR., JUAN G.
;  APPLICANT:  HOOGEVEEN, RON C.
;  APPLICANT:  MOORE, PAUL J.
;  TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID VECTORS
;  FILE REFERENCE: ARAG:003USD1
;  CURRENT APPLICATION NUMBER: US/10/656,053B
;  CURRENT FILING DATE:  2003-09-05
;  PRIOR APPLICATION NUMBER: 09/079,030
;  PRIOR FILING DATE: 1998-05-14
;  PRIOR APPLICATION NUMBER: 08/874,807
;  PRIOR FILING DATE: 1997-06-13
;  NUMBER OF SEQ ID NOS: 229
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4536
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-656-053B-1

  Query Match            100.0%;  Score 102;  DB 5;  Length 4536;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        661 IEIGLEGKGFEPTLEALFGK 680


RESULT 5
US-10-398-200-2
; Sequence 2, Application US/10398200
; Publication No. US20050048062A1
; GENERAL INFORMATION:
;  APPLICANT: AGNELLO, VINCENT
;  TITLE OF INVENTION: METHOD OF INHIBITING INFECTION BY HCV, OTHER
;  TITLE OF INVENTION:  FLAVIVIRIDAE VIRUSES, AND ANY OTHER VIRUS THAT
;  TITLE OF INVENTION:  COMPLEXES TO LOW DENSITY LIPOPROTEIN OR TO VERY LOW
;  TITLE OF INVENTION:  DENSITY LIPOPRTOEIN IN BLOOD BY PREVENTING VIRAL ENTRY
;  TITLE OF INVENTION:  INTO A CELL
;  FILE REFERENCE: 1513-PCT-00
;  CURRENT APPLICATION NUMBER: US/10/398,200
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/243,594
;  PRIOR FILING DATE: 2000-10-25
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4560
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-398-200-2

  Query Match            100.0%;  Score 102;  DB 5;  Length 4560;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        685 IEIGLEGKGFEPTLEALFGK 704


RESULT 6
US-09-870-759-128
; Sequence 128, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: 870759
;  CURRENT APPLICATION NUMBER: US/09/870,759
;  CURRENT FILING DATE:  2002-01-14
;  PRIOR APPLICATION NUMBER: US 60/208,128
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 166
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-870-759-128

  Query Match            100.0%;  Score 102;  DB 3;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 7
US-09-802-640-32
; Sequence 32, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bonsal Aruna
;  APPLICANT:  Kleyn Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048
;  CURRENT APPLICATION NUMBER: US/09/802,640
;  CURRENT FILING DATE:  2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-802-640-32

  Query Match             100.0%;  Score 102;  DB 3;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 8
US-09-751-708A-128
; Sequence 128, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: 751708
;  CURRENT APPLICATION NUMBER: US/09/751,708A
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: US 60/173,371
;  PRIOR FILING DATE: 1999-12-28
;  NUMBER OF SEQ ID NOS: 166
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-751-708A-128

  Query Match             100.0%;  Score 102;  DB 3;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 9
US-10-403-902A-32
; Sequence 32, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
;  APPLICANT: Braun, Andreas
;  APPLICANT:  Bansal, Aruna
;  APPLICANT:  Kleyn, Patrick
;  TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  CARDIOVASCULAR DISEASE AND THEIR USE
;  FILE REFERENCE: 24736-2048B
;  CURRENT APPLICATION NUMBER: US/10/403,902A
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: 09/802,640
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-403-902A-32

  Query Match             100.0%;  Score 102;  DB 4;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 10
US-10-741-601-432
; Sequence 432, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 432
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-601-432

  Query Match             100.0%;  Score 102;  DB 4;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 11
US-10-741-601-433
; Sequence 433, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 433
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-601-433

  Query Match             100.0%;  Score 102;  DB 4;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
```

```
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 12
US-10-428-817A-124
; Sequence 124, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
;  APPLICANT: TERMAN, David S
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
;  FILE REFERENCE: 38373-189118
;  CURRENT APPLICATION NUMBER: US/10/428,817A
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: US 60/378,988
;  PRIOR FILING DATE: 2002-05-08
;  PRIOR APPLICATION NUMBER: US 60/389,366
;  PRIOR FILING DATE: 2002-06-15
;  PRIOR APPLICATION NUMBER: US 60/406,697
;  PRIOR FILING DATE: 2002-08-28
;  PRIOR APPLICATION NUMBER: US 60/406,750
;  PRIOR FILING DATE: 2002-08-29
;  PRIOR APPLICATION NUMBER: US 60/415,310
;  PRIOR FILING DATE: 2002-10-01
;  PRIOR APPLICATION NUMBER: US 60/415,400
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: US 60/438,686
;  PRIOR FILING DATE: 2003-01-09
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-428-817A-124

  Query Match             100.0%;  Score 102;  DB 4;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 13
US-10-741-600-1287
; Sequence 1287, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1287
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1287

  Query Match             100.0%;  Score 102;  DB 5;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 14
US-10-741-600-1288
; Sequence 1288, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1288
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-741-600-1288

  Query Match             100.0%;  Score 102;  DB 5;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 15
US-10-868-577A-25
; Sequence 25, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo et al.
;  TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
;  FILE REFERENCE: 28967/39359A
;  CURRENT APPLICATION NUMBER: US/10/868,577A
;  CURRENT FILING DATE:  2004-06-14
;  PRIOR APPLICATION NUMBER: US 60/478,390
;  PRIOR FILING DATE: 2003-06-12
;  PRIOR APPLICATION NUMBER: US 10/669,176
;  PRIOR FILING DATE: 2003-09-23
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
;   LENGTH: 4563
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (32)..(126)
;   OTHER INFORMATION: heparin binding domain
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3161)..(3236)
;   OTHER INFORMATION: heparin binding domain
US-10-868-577A-25

  Query Match             100.0%;  Score 102;  DB 5;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


Search completed: March 21, 2006, 19:11:02
Job time : 166 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:08:23 ; Search time 22 Seconds
(without alignments)
26.021 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	45.1	326	7	US-11-087-099-7879	Sequence 7879, Ap
2	44	43.1	387	7	US-11-087-099-976	Sequence 976, App
3	44	43.1	387	7	US-11-087-099-6374	Sequence 6374, Ap
4	44	43.1	387	7	US-11-087-099-9490	Sequence 9490, Ap
5	44	43.1	387	7	US-11-087-099-11913	Sequence 11913, A
6	43	42.2	1516	6	US-10-220-824-8	Sequence 8, Appli
7	42	41.2	321	7	US-11-096-568A-10658	Sequence 10658, A
8	42	41.2	321	7	US-11-096-568A-14981	Sequence 14981, A
9	42	41.2	426	7	US-11-096-568A-10657	Sequence 10657, A
10	42	41.2	428	7	US-11-096-568A-14980	Sequence 14980, A
11	42	41.2	454	7	US-11-096-568A-10656	Sequence 10656, A
12	41.5	40.7	506	7	US-11-142-700-20	Sequence 20, Appl
13	41.5	40.7	701	7	US-11-142-700-28	Sequence 28, Appl
14	41.5	40.7	964	7	US-11-096-568A-27029	Sequence 27029, A
15	41.5	40.7	969	7	US-11-096-568A-27028	Sequence 27028, A
16	41.5	40.7	1077	7	US-11-096-568A-27027	Sequence 27027, A
17	41	40.2	137	6	US-10-793-626-1980	Sequence 1980, Ap
18	41	40.2	233	7	US-11-098-686-11302	Sequence 11302, A
19	41	40.2	327	7	US-11-087-099-6121	Sequence 6121, Ap
20	41	40.2	327	7	US-11-087-099-11014	Sequence 11014, A
21	41	40.2	1147	6	US-10-453-372-4	Sequence 4, Appli
22	41	40.2	1179	6	US-10-912-580-1	Sequence 1, Appli
23	41	40.2	1181	6	US-10-912-580-2	Sequence 2, Appli
24	41	40.2	1181	6	US-10-912-580-3	Sequence 3, Appli
25	40	39.2	190	6	US-10-467-657-2540	Sequence 2540, Ap
26	40	39.2	201	7	US-11-096-568A-26965	Sequence 26965, A
27	40	39.2	233	7	US-11-096-568A-26964	Sequence 26964, A
28	40	39.2	387	7	US-11-087-099-8098	Sequence 8098, Ap
29	40	39.2	637	7	US-11-087-099-4885	Sequence 4885, Ap
30	40	39.2	793	7	US-11-087-099-9278	Sequence 9278, Ap
31	39	38.2	334	7	US-11-087-099-8950	Sequence 8950, Ap
32	39	38.2	391	6	US-10-878-556A-86	Sequence 86, Appl
33	39	38.2	449	7	US-11-072-512-2749	Sequence 2749, Ap
34	39	38.2	464	7	US-11-098-686-11345	Sequence 11345, A
35	39	38.2	518	6	US-10-467-657-1124	Sequence 1124, Ap
36	39	38.2	657	7	US-11-110-082-37	Sequence 37, Appl
37	39	38.2	798	7	US-11-110-082-39	Sequence 39, Appl
38	38.5	37.7	260	7	US-11-096-568A-24339	Sequence 24339, A
39	38.5	37.7	262	7	US-11-054-281-89	Sequence 89, Appl
40	38.5	37.7	266	7	US-11-054-281-88	Sequence 88, Appl
41	38.5	37.7	290	7	US-11-096-568A-24338	Sequence 24338, A
42	38.5	37.7	294	7	US-11-054-281-87	Sequence 87, Appl
43	38.5	37.7	312	7	US-11-054-281-20	Sequence 20, Appl
44	38.5	37.7	312	7	US-11-054-281-86	Sequence 86, Appl
45	38.5	37.7	327	7	US-11-096-568A-24337	Sequence 24337, A

ALIGNMENTS

RESULT 1
US-11-087-099-7879
; Sequence 7879, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7879
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Lactococcus lactis subsp. lactis
US-11-087-099-7879

Query Match 45.1%; Score 46; DB 7; Length 326;
Best Local Similarity 52.9%; Pred. No. 5.9;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          3 IGLEGKGFEPTLEALFG 19
              |||  :|| | :|  ||
Db         68 IGLATQGFHPIMEIQFG 84
```

RESULT 2
US-11-087-099-976
; Sequence 976, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 976
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Gaeumannomyces graminis var. tritici
US-11-087-099-976

Query Match 43.1%; Score 44; DB 7; Length 387;
Best Local Similarity 46.2%; Pred. No. 15;
Matches 12; Conservative 2; Mismatches 6; Indels 6; Gaps 1;

```
Qy          1 IEIGLEG------KGFEPTLEALFGK 20
```

```
              || ||:         | ||||: |||
Db        290 IEAGLDMNMPGPLNFFAPTLESYFGK 315


RESULT 3
US-11-087-099-6374
; Sequence 6374, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6374
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Gaeumannomyces graminis var. graminis
US-11-087-099-6374

  Query Match             43.1%;  Score 44;  DB 7;  Length 387;
  Best Local Similarity   46.2%;  Pred. No. 15;
  Matches   12;  Conservative    2;  Mismatches    6;  Indels    6;  Gaps    1;

Qy          1 IEIGLEG------KGFEPTLEALFGK 20
              || ||:         | ||||: |||
Db        290 IEAGLDMNMPGPLNFFAPTLESYFGK 315


RESULT 4
US-11-087-099-9490
; Sequence 9490, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9490
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Gaeumannomyces graminis var. tritici
US-11-087-099-9490

  Query Match             43.1%;  Score 44;  DB 7;  Length 387;
  Best Local Similarity   46.2%;  Pred. No. 15;
  Matches   12;  Conservative    2;  Mismatches    6;  Indels    6;  Gaps    1;

Qy          1 IEIGLEG------KGFEPTLEALFGK 20
              || ||:         | ||||: |||
Db        290 IEAGLDMNMPGPLNFFAPTLESYFGK 315


RESULT 5
US-11-087-099-11913
; Sequence 11913, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11913
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Gaeumannomyces graminis var. tritici
US-11-087-099-11913

  Query Match             43.1%;  Score 44;  DB 7;  Length 387;
  Best Local Similarity   46.2%;  Pred. No. 15;
  Matches   12;  Conservative    2;  Mismatches    6;  Indels    6;  Gaps    1;

Qy          1 IEIGLEG------KGFEPTLEALFGK 20
              || ||:         | ||||: |||
Db        290 IEAGLDMNMPGPLNFFAPTLESYFGK 315


RESULT 6
US-10-220-824-8
; Sequence 8, Application US/10220824
; Publication No. US20050277603A1
; GENERAL INFORMATION:
;  APPLICANT: ViroMed Limited
;  TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a
;  TITLE OF INVENTION:  gene encoding an anti-angiogenic protein or parts thereof
;  FILE REFERENCE: OPF0208/PCT
;  CURRENT APPLICATION NUMBER: US/10/220,824
;  CURRENT FILING DATE:  2002-08-30
;  PRIOR APPLICATION NUMBER: KR 2001-0000691
;  PRIOR FILING DATE: 2001-01-05
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: KopatentIn 1.71
; SEQ ID NO 8
;   LENGTH: 1516
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-220-824-8

  Query Match             42.2%;  Score 43;  DB 6;  Length 1516;
  Best Local Similarity   58.8%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFEPTLEALFG 19
              | :|| ||   |||| |
Db        649 IDMEGSGFGGDLEALRG 665


RESULT 7
US-11-096-568A-10658
; Sequence 10658, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10658
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(321)
;   OTHER INFORMATION: Ceres Seq. ID no. 13596806
US-11-096-568A-10658

  Query Match             41.2%;  Score 42;  DB 7;  Length 321;
  Best Local Similarity   53.8%;  Pred. No. 26;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTL 14
              ::| ||| | ||:
Db         18 KVGAEGKRFRPTV 30


RESULT 8
US-11-096-568A-14981
; Sequence 14981, Application US/11096568A
```

```
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14981
;   LENGTH: 321
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(321)
;   OTHER INFORMATION: Ceres Seq. ID no. 12341338
US-11-096-568A-14981

  Query Match             41.2%;  Score 42;  DB 7;  Length 321;
  Best Local Similarity   53.8%;  Pred. No. 26;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTL 14
              ::| ||| | ||:
Db         18 KVGAEGKRFRPTV 30


RESULT 9
US-11-096-568A-10657
; Sequence 10657, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10657
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(426)
;   OTHER INFORMATION: Ceres Seq. ID no. 13596805
US-11-096-568A-10657

  Query Match             41.2%;  Score 42;  DB 7;  Length 426;
  Best Local Similarity   53.8%;  Pred. No. 36;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTL 14
              ::| ||| | ||:
Db        123 KVGAEGKRFRPTV 135


RESULT 10
US-11-096-568A-14980
; Sequence 14980, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14980
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(428)
;   OTHER INFORMATION: Ceres Seq. ID no. 12341337
US-11-096-568A-14980

  Query Match             41.2%;  Score 42;  DB 7;  Length 428;
  Best Local Similarity   53.8%;  Pred. No. 36;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTL 14
              ::| ||| | ||:
Db        125 KVGAEGKRFRPTV 137


RESULT 11
US-11-096-568A-10656
; Sequence 10656, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10656
;   LENGTH: 454
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(454)
;   OTHER INFORMATION: Ceres Seq. ID no. 13596804
US-11-096-568A-10656

  Query Match             41.2%;  Score 42;  DB 7;  Length 454;
  Best Local Similarity   53.8%;  Pred. No. 39;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTL 14
              ::| ||| | ||:
Db        151 KVGAEGKRFRPTV 163


RESULT 12
US-11-142-700-20
; Sequence 20, Application US/11142700
; Publication No. US20060026721A1
; GENERAL INFORMATION:
;  APPLICANT: Stephen M. Allen
;  APPLICANT:  Gary M. Fader
;  APPLICANT:  Saverio Carl Falco
;  APPLICANT:  Anthony J. Kinney
;  APPLICANT:  Jonathan E. Lightner
;  APPLICANT:  Guo-Hua Miao
;  APPLICANT:  J. Antoni Rafalski
;  APPLICANT:  Catherine J. Thorpe
;  TITLE OF INVENTION: Plant Cellulose Synthases
;  FILE REFERENCE: BB-1170
;  CURRENT APPLICATION NUMBER: US/11/142,700
;  CURRENT FILING DATE:  2005-06-01
;  PRIOR APPLICATION NUMBER: US/09/720,383
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/092,844
;  PRIOR FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
;   LENGTH: 506
```

```
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (88)
;   OTHER INFORMATION: Xaa = any amino acid
US-11-142-700-20

  Query Match             40.7%;  Score 41.5;  DB 7;  Length 506;
  Best Local Similarity   37.9%;  Pred. No. 53;
  Matches   11;  Conservative    4;  Mismatches    5;  Indels    9;  Gaps    1;

Qy          1 IEIGLEGKGFEP---------TLEALFGK 20
              || |:|| ||:         :||  ||:
Db        122 IEEGVEGAGFDDEKSVLMSQMSLEKRFGQ 150


RESULT 13
US-11-142-700-28
; Sequence 28, Application US/11142700
; Publication No. US20060026721A1
; GENERAL INFORMATION:
;  APPLICANT: Stephen M. Allen
;  APPLICANT:  Gary M. Fader
;  APPLICANT:  Saverio Carl Falco
;  APPLICANT:  Anthony J. Kinney
;  APPLICANT:  Jonathan E. Lightner
;  APPLICANT:  Guo-Hua Miao
;  APPLICANT:  J. Antoni Rafalski
;  APPLICANT:  Catherine J. Thorpe
;  TITLE OF INVENTION: Plant Cellulose Synthases
;  FILE REFERENCE: BB-1170
;  CURRENT APPLICATION NUMBER: US/11/142,700
;  CURRENT FILING DATE:  2005-06-01
;  PRIOR APPLICATION NUMBER: US/09/720,383
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/092,844
;  PRIOR FILING DATE: 1998-07-14
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 28
;   LENGTH: 701
;   TYPE: PRT
;   ORGANISM: Gossypium hirsutum
US-11-142-700-28

  Query Match             40.7%;  Score 41.5;  DB 7;  Length 701;
  Best Local Similarity   37.9%;  Pred. No. 78;
  Matches   11;  Conservative    4;  Mismatches    5;  Indels    9;  Gaps    1;

Qy          1 IEIGLEGKGFEP---------TLEALFGK 20
              || |:|| ||:         :||  ||:
Db        317 IEEGVEGAGFDDEKSLLMSQMSLEKRFGQ 345


RESULT 14
US-11-096-568A-27029
; Sequence 27029, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27029
;   LENGTH: 964
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(964)
;   OTHER INFORMATION: Ceres Seq. ID no. 13666076
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (381)..(381)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-27029

  Query Match             40.7%;  Score 41.5;  DB 7;  Length 964;
  Best Local Similarity   37.9%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    4;  Mismatches    5;  Indels    9;  Gaps    1;

Qy          1 IEIGLEGKGFEP---------TLEALFGK 20
              || |:|| ||:         :||  ||:
Db        580 IEEGVEGAGFDDEKSLLMSQMSLEKRFGQ 608


RESULT 15
US-11-096-568A-27028
; Sequence 27028, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27028
;   LENGTH: 969
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(969)
;   OTHER INFORMATION: Ceres Seq. ID no. 13666075
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (386)..(386)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-27028

  Query Match             40.7%;  Score 41.5;  DB 7;  Length 969;
  Best Local Similarity   37.9%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    4;  Mismatches    5;  Indels    9;  Gaps    1;

Qy          1 IEIGLEGKGFEP---------TLEALFGK 20
              || |:|| ||:         :||  ||:
Db        585 IEEGVEGAGFDDEKSLLMSQMSLEKRFGQ 613


Search completed: March 21, 2006, 19:11:30
Job time : 22 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:11:18 ; Search time 182 Seconds
(without alignments)
48.283 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 37136

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	20	6	AAE34006	Aae34006 Human apo
2	102	100.0	20	8	ADN00563	Adn00563 Apolipopr
3	102	100.0	20	8	ADM98203	Adm98203 Apolipopr
4	36	35.3	20	9	ADY28584	Ady28584 Novel mod
5	32	31.4	20	4	AAM18133	Aam18133 Peptide #
6	32	31.4	20	4	ABB37163	Abb37163 Peptide #
7	32	31.4	20	4	ABG51999	Abg51999 Human liv
8	31	30.4	20	9	ADY28585	Ady28585 Novel mod
9	30	29.4	20	6	ADA51189	Ada51189 Vesicular
10	30	29.4	20	8	ADU20808	Adu20808 Random st
11	29	28.4	20	6	AAE37248	Aae37248 Hevea bra
12	29	28.4	20	7	ADH47596	Adh47596 Human lun
13	29	28.4	20	8	ADJ21515	Adj21515 Human lun
14	28.5	27.9	20	4	AAY72709	Aay72709 Parvoviru
15	28	27.5	20	2	AAW34804	Aaw34804 Arg-speci
16	28	27.5	20	6	ADA51188	Ada51188 Vesicular
17	28	27.5	20	9	ADY32591	Ady32591 Viral dis
18	28	27.5	20	9	ADY32588	Ady32588 Viral dis
19	28	27.5	20	9	ADY32589	Ady32589 Viral dis
20	28	27.5	20	9	ADY32593	Ady32593 Viral dis
21	28	27.5	20	9	ADY32595	Ady32595 Viral dis
22	28	27.5	20	9	ADY32594	Ady32594 Viral dis
23	28	27.5	20	9	ADY32590	Ady32590 Viral dis
24	28	27.5	20	9	ADY32592	Ady32592 Viral dis
25	27	26.5	20	2	AAR39826	Aar39826 E1 peptid
26	27	26.5	20	5	AAU80402	Aau80402 Human L58
27	27	26.5	20	5	AAU90670	Aau90670 Insulin/i
28	27	26.5	20	6	ABP55288	Abp55288 Human adr
29	27	26.5	20	6	ADA04507	Ada04507 Insulin r
30	27	26.5	20	7	ADB95144	Adb95144 Human lun
31	27	26.5	20	7	ADH95720	Adh95720 Insulin r
32	27	26.5	20	8	ADJ92852	Adj92852 Co-activa
33	27	26.5	20	8	ADL68411	Adl68411 IGF-1R/IR
34	27	26.5	20	8	ADM38256	Adm38256 Anti-IR m
35	26.5	26.0	20	3	AAB26099	Aab26099 P5 mimoto
36	26.5	26.0	20	3	AAB23436	Aab23436 Human IgE
37	26.5	26.0	20	4	AAU16824	Aau16824 Peptide P
38	26.5	26.0	20	5	ABJ00445	Abj00445 Human IgE
39	26	25.5	20	2	AAW02262	Aaw02262 Gingivali
40	26	25.5	20	2	AAW82211	Aaw82211 Fluorogen
41	26	25.5	20	3	AAB34393	Aab34393 Human sec
42	26	25.5	20	3	AAB39138	Aab39138 Human sec
43	26	25.5	20	4	AAG73229	Aag73229 Protease
44	26	25.5	20	4	AAB35173	Aab35173 Human Tra
45	26	25.5	20	5	AAE21737	Aae21737 BSMR effe

ALIGNMENTS

RESULT 1
AAE34006
ID AAE34006 standard; peptide; 20 AA.
XX
AC AAE34006;
XX
DT 02-MAY-2003 (first entry)
XX
DE Human apo-lipoprotein B peptide #32.
XX
KW Human; immunostimulant; apo-lipoprotein B; apoB; myocardial infarction;
KW vaccine; ischaemic cardiovascular disease; inflammation; cell toxicity;
KW atherosclerosis; therapy.
XX
OS Homo sapiens.
XX
PN WO200280954-A1.
XX
PD 17-OCT-2002.
XX
PF 05-APR-2002; 2002WO-SE000679.
XX
PR 05-APR-2001; 2001SE-00001232.
PR 09-NOV-2001; 2001SE-00003754.
XX
PA (FORS-) FORSKARPATENT I SYD.
XX
PI Nilsson J, Shah PK;
XX
DR WPI; 2003-140132/13.
XX
PT New fragments of apo-lipoprotein B, useful for treatment, prevention and
PT diagnosis of ischemic cardiovascular disease and atherosclerosis.
XX
PS Claim 4; Page 33; 60pp; English.
XX
CC The invention relates to fragments of human apo-lipoprotein B (apoB).
CC ApoB peptides are useful for immunisation or treatment of ischaemic
CC cardiovascular diseases and for diagnosing the presence or absence of
CC antibodies related to increased or decreased risk of developing
CC cardiovascular diseases. They are useful for treating myocardial
CC infarction and unstable atherosclerotic plaques in which oxidised low-
CC density lipoprotein may contribute to inflammation, cell toxicity and
CC risk of plaque rupture. They are also useful as vaccines. The present
CC sequence is human apoB peptide
XX
SQ Sequence 20 AA;

```
  Query Match             100.0%;  Score 102;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 2
ADN00563
ID   ADN00563 standard; peptide; 20 AA.
XX
AC   ADN00563;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Apolipoprotein B oxidised peptide fragment.
XX
KW   human antibody; antibody; apolipoprotein B; atherosclerosis;
KW   passive immunisation; antiarteriosclerotic;
KW   anti-apolipoprotein B antibody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004030698-A1.
XX
PD   15-APR-2004.
XX
PF   22-SEP-2003; 2003WO-SE001469.
XX
PR   04-OCT-2002; 2002SE-00002959.
PR   27-AUG-2003; 2003SE-00002312.
XX
PA   (FORS-) FORSKARPATENT I SYD AB.
XX
PI   Nilsson J,  Carlsson R,  Bengtsson J,  Strandberg L;
XX
DR   WPI; 2004-316343/29.
XX
PT   Use of a recombinant human antibody or antibody fragment directed towards
PT   at least one oxidized fragment of apolipoprotein B for the manufacture of
PT   a pharmaceutical composition for treating atherosclerosis.
XX
PS   Claim 2; Page 26; 59pp; English.
XX
CC   The present invention describes the use of at least one recombinant human
CC   antibody or antibody fragment directed towards at least one oxidised
CC   fragment of apolipoprotein B in the manufacture of a pharmaceutical
CC   composition for treatment of atherosclerosis by means of passive
CC   immunisation. Also described: (1) preparing the isolated antibody; (2)
CC   amplification of isolated human antibody; (3) passive immunisation of
CC   mammals; and (4) a pharmaceutical composition comprising the recombinant
CC   human antibody directed towards at least one oxidised fragment of
CC   apolipoprotein B for treatment of atherosclerosis by means of passive
CC   immunisation. The human antibody has antiarteriosclerotic activity. The
CC   isolated human antibody or antibody fragment directed towards at least
CC   one oxidised fragment of apolipoprotein B is useful in the manufacture of
CC   a pharmaceutical composition for treatment of atherosclerosis by means of
CC   passive immunisation. The present sequence represents an oxidised
CC   fragment of apolipoprotein B, which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 102;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 3
ADM98203
ID   ADM98203 standard; peptide; 20 AA.
XX
AC   ADM98203;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Apolipoprotein B oxidised peptide fragment.
XX
KW   human antibody; antibody; apolipoprotein B; atherosclerosis;
KW   passive immunisation; antiarteriosclerotic.
XX
OS   Homo sapiens.
XX
PN   WO2004030607-A2.
XX
PD   15-APR-2004.
XX
PF   06-OCT-2003; 2003WO-SE001547.
XX
PR   04-OCT-2002; 2002SE-00002959.
PR   27-AUG-2003; 2003SE-00002312.
PR   22-SEP-2003; 2003WO-SE001469.
XX
PA   (FORS-) FORSKARPATENT I SYD AB.
XX
PI   Nilsson J,  Carlsson R,  Bengtsson J,  Strandberg L;
XX
DR   WPI; 2004-316320/29.
XX
PT   Use of an isolated human antibody or antibody fragment directed towards
PT   at least one oxidized fragment of apolipoprotein B in the manufacture of
PT   a pharmaceutical composition for treating atherosclerosis.
XX
PS   Claim 2; Page 26; 84pp; English.
XX
CC   The present invention describes the use of at least one isolated human
CC   antibody or antibody fragment directed towards at least one oxidised
CC   fragment of apolipoprotein B in the manufacture of a pharmaceutical
CC   composition for treatment of atherosclerosis by means of passive
CC   immunisation. Also described: (1) preparing the isolated antibody; (2)
CC   amplifying the isolated human antibody; (3) passive immunisation of
CC   mammals; and (4) a pharmaceutical composition comprising the isolated
CC   human antibody directed towards at least one oxidised fragment of
CC   apolipoprotein B for treatment of atherosclerosis by means of passive
CC   immunisation, where the antibody is present in combination with a
CC   pharmaceutical excipient. The human antibody has antiarteriosclerotic
CC   activity. The isolated human antibody or antibody fragment directed
CC   towards at least one oxidised fragment of apolipoprotein B is useful in
CC   the manufacture of a pharmaceutical composition for treatment of
CC   atherosclerosis by means of passive immunisation. The present sequence
CC   represents an oxidised apolipoprotein B peptide fragment, which is used
CC   in the exemplification of the present invention.
XX
SQ   Sequence 20 AA;

  Query Match             100.0%;  Score 102;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-10;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 4
ADY28584
ID   ADY28584 standard; peptide; 20 AA.
XX
```

```
AC   ADY28584;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Novel modified viral particle-related SIVmac 239 gag peptide SeqID42.
XX
KW   virus-like particle; immune stimulation; virucide; anti-HIV; vaccine;
KW   gene therapy; viral infection; HIV infection; gag.
XX
OS   Simian immunodeficiency virus SIVmac.
XX
PN   WO2005016246-A2.
XX
PD   24-FEB-2005.
XX
PF   21-JUN-2004; 2004WO-US019739.
XX
PR   20-JUN-2003; 2003US-00601656.
PR   01-AUG-2003; 2003US-0491928P.
PR   31-DEC-2003; 2003US-0533542P.
PR   09-FEB-2004; 2004US-0542947P.
XX
PA   (LIPI-) LIPID SCI INC.
XX
PI   Cham BE,  Maltais JB,  Bellotti M;
XX
DR   WPI; 2005-173215/18.
XX
PT   New modified viral particles with immunogenic properties and reduced
PT   lipid content, useful for preventing and treating infectious viral
PT   diseases, such as HIV.
XX
PS   Example 3; SEQ ID NO 42; 111pp; English.
XX
CC   This invention relates to a novel modified viral particle comprising at
CC   least a partially reduced lipid content viral particle, where the viral
CC   particle initiates a positive immune response in a patient and incites
CC   protection in the patient against an infectious organism. The invention
CC   may be useful for the development of compounds with a virucide or anti-
CC   HIV activity or the production of a vaccine. The disclosed sequences may
CC   prove useful for gene therapy. The modified viral particle is useful for
CC   preparing a medicament that provides protection in a patient against an
CC   infectious viral organism following administration of the medicament to
CC   the patient. The invention may also be used for treating viral
CC   infections, such as HIV. The present sequence is that of an SIVmac 239
CC   gag peptide which was used during the exemplification of the invention.
XX
SQ   Sequence 20 AA;

  Query Match             35.3%;  Score 36;  DB 9;  Length 20;
  Best Local Similarity   53.8%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LEGKGFEPTLEAL 17
              |:| |  |||| :
Db          7 LKGLGVNPTLEEM 19


RESULT 5
AAM18133
ID   AAM18133 standard; protein; 20 AA.
XX
AC   AAM18133;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Peptide #4567 encoded by probe for measuring cervical gene expression.
XX
KW   Probe; human; microarray; gene expression; cervical epithelial cell;
KW   cervical cancer.
XX
OS   Homo sapiens.
XX
PN   WO200157278-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000670.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
PR   04-OCT-2000; 2000GB-00024263.
XX
PA   (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI   Penn SG,  Hanzel DK,  Chen W,  Rank DR;
XX
DR   WPI; 2001-488901/53.
XX
PT   Human genome-derived single exon nucleic acid probes useful for analyzing
PT   gene expression in human cervical epithelial cells.
XX
PS   Claim 27; SEQ ID NO 22959; 487pp; English.
XX
CC   The present invention relates to human single exon nucleic acid probes
CC   (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC   by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC   can be used to produce a single exon microarray, which can be used for
CC   measuring human gene expression in a sample derived from human cervical
CC   epithelial cells. By measuring gene expression, the probes are therefore
CC   useful in grading and/or staging of diseases of the cervix, notably
CC   cervical cancer. Note: The sequence data for this patent did not form
CC   part of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 AA;

  Query Match             31.4%;  Score 32;  DB 4;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5.4e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 6
ABB37163
ID   ABB37163 standard; peptide; 20 AA.
XX
AC   ABB37163;
XX
DT   04-FEB-2002  (first entry)
XX
DE   Peptide #4669 encoded by human foetal liver single exon probe.
XX
KW   Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS   Homo sapiens.
XX
PN   WO200157277-A2.
XX
PD   09-AUG-2001.
XX
PF   30-JAN-2001; 2001WO-US000669.
XX
PR   04-FEB-2000; 2000US-0180312P.
PR   26-MAY-2000; 2000US-0207456P.
PR   30-JUN-2000; 2000US-00608408.
PR   03-AUG-2000; 2000US-00632366.
PR   21-SEP-2000; 2000US-0234687P.
PR   27-SEP-2000; 2000US-0236359P.
```

PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 29798; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 31.4%; Score 32; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEP 12
: | || || :|
Db 2 LHIKLEAKGLKP 13

RESULT 7
ABG51999
ID ABG51999 standard; peptide; 20 AA.
XX
AC ABG51999;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 30647.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488898/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 30647; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 31.4%; Score 32; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEP 12
: | || || :|
Db 2 LHIKLEAKGLKP 13

RESULT 8
ADY28585
ID ADY28585 standard; peptide; 20 AA.
XX
AC ADY28585;
XX
DT 05-MAY-2005 (first entry)
XX
DE Novel modified viral particle-related SIVmac 239 gag peptide SeqID43.
XX
KW virus-like particle; immune stimulation; virucide; anti-HIV; vaccine;
KW gene therapy; viral infection; HIV infection; gag.
XX
OS Simian immunodeficiency virus SIVmac.
XX
PN WO2005016246-A2.
XX
PD 24-FEB-2005.
XX
PF 21-JUN-2004; 2004WO-US019739.
XX
PR 20-JUN-2003; 2003US-00601656.
PR 01-AUG-2003; 2003US-0491928P.
PR 31-DEC-2003; 2003US-0533542P.
PR 09-FEB-2004; 2004US-0542947P.
XX
PA (LIPI-) LIPID SCI INC.
XX
PI Cham BE, Maltais JB, Bellotti M;
XX
DR WPI; 2005-173215/18.
XX
PT New modified viral particles with immunogenic properties and reduced
PT lipid content, useful for preventing and treating infectious viral
PT diseases, such as HIV.
XX
PS Example 3; SEQ ID NO 43; 111pp; English.
XX
CC This invention relates to a novel modified viral particle comprising at
CC least a partially reduced lipid content viral particle, where the viral
CC particle initiates a positive immune response in a patient and incites
CC protection in the patient against an infectious organism. The invention
CC may be useful for the development of compounds with a virucide or anti-
CC HIV activity or the production of a vaccine. The disclosed sequences may
CC prove useful for gene therapy. The modified viral particle is useful for
CC preparing a medicament that provides protection in a patient against an
CC infectious viral organism following administration of the medicament to

```
CC   the patient. The invention may also be used for treating viral
CC   infections, such as HIV. The present sequence is that of an SIVmac 239
CC   gag peptide which was used during the exemplification of the invention.
XX
SQ   Sequence 20 AA;

  Query Match             30.4%;  Score 31;  DB 9;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 8e+02;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 GKGFEPTLEAL 17
              | |  |||| :
Db          1 GLGVNPTLEEM 11


RESULT 9
ADA51189
ID   ADA51189 standard; peptide; 20 AA.
XX
AC   ADA51189;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Vesicular stomatitis virus matrix protein peptide fragment SEQ ID NO:438.
XX
KW   PPXY motif; type I WW-domain; Nedd4; virucide; viral budding;
KW   virus propagation; viral infection; hepatitis B virus;
KW   human herpes virus 1; matrix protein.
XX
OS   Vesicular stomatitis virus.
XX
PN   WO2003015714-A2.
XX
PD   27-FEB-2003.
XX
PF   21-AUG-2002; 2002WO-US026681.
XX
PR   21-AUG-2001; 2001US-0313883P.
XX
PA   (MYRI-) MYRIAD GENETICS INC.
XX
PI   Morham S,  Zavitz K,  Hobden A;
XX
DR   WPI; 2003-300559/29.
XX
PT   Novel peptide capable of binding to type I WW-domain of Nedd4 protein and
PT   useful for treating viral infections, comprises contiguous amino acid
PT   sequence of a viral protein encompassing PPXY motif.
XX
PS   Claim 19; Page 44; 75pp; English.
XX
CC   The invention relates to a novel isolated peptide comprising a contiguous
CC   amino acid sequence of 8-30 amino acid residues of a viral protein, where
CC   the contiguous amino acid sequence encompasses the PPXY motif of the
CC   viral protein and the peptide is capable of binding a type I WW-domain of
CC   the Nedd4 protein. A peptide of the invention has virucide activity, and
CC   acts as an inhibitor of viral budding and virus propagation. The peptides
CC   are useful in the manufacture of a medicament useful in the treatment of
CC   viral infections caused by a virus selected from hepatitis B virus and
CC   human herpes virus 1. The peptides are also useful for inhibiting viral
CC   budding from virus-infected cells and thus inhibiting virus propagation
CC   in the cells. The present sequence represents a peptide of the invention.
XX
SQ   Sequence 20 AA;

  Query Match             29.4%;  Score 30;  DB 6;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IGLEGKG 9
              :||:|||
Db          1 LGLKGKG 7


RESULT 10
ADU20808
ID   ADU20808 standard; peptide; 20 AA.
XX
AC   ADU20808;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Random starting clone used in Abeta adhesion screening.
XX
KW   Abeta; amyloid beta; amyloid; Alzheimer's disease; neuroprotective;
KW   nootropic.
XX
OS   Unidentified.
XX
PN   WO2004092197-A2.
XX
PD   28-OCT-2004.
XX
PF   07-APR-2004; 2004WO-US010939.
XX
PR   07-APR-2003; 2003US-0461168P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Martin PT;
XX
DR   WPI; 2004-766825/75.
XX
PT   New polypeptides that interact with amyloid plaques containing amyloid
PT   beta peptides for diagnosing or treating neurodegenerative diseases
PT   associated with aberrant plaque formation (e.g. Alzheimer's disease).
XX
PS   Example; SEQ ID NO 13; 52pp; English.
XX
CC   The invention relates to an isolated polypeptide that interacts with
CC   amyloid plaques containing amyloid beta (Abeta) peptide. The peptide
CC   binds to the amyloid form of the Abeta1-40 peptide in plaques of
CC   Alzheimer's disease patients. The polypeptide can be prepared using
CC   standard isolation techniques. Compositions comprising the peptide and
CC   methods are useful for diagnosing or treating neurodegenerative diseases
CC   associated with aberrant plaque formation (e.g. Alzheimer's disease).
CC   Sequences ADU20802 -ADU20811 represent sequences of 10 randomly picked
CC   phage clones in the starting library that were screened for
CC   identification of peptides that adhere to amyloid form of the Abeta
CC   peptide.
XX
SQ   Sequence 20 AA;

  Query Match             29.4%;  Score 30;  DB 8;  Length 20;
  Best Local Similarity   57.1%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GLEGKGF 10
              |:||:|:
Db          4 GMEGRGY 10


RESULT 11
AAE37248
ID   AAE37248 standard; peptide; 20 AA.
XX
AC   AAE37248;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Hevea brasiliensis Hev b 6 peptide #17.
XX
KW   Immunological; latex allergy; plant; immune response; hypersensitivity;
KW   rubber plant; Hev b 6; therapy.
XX
OS   Hevea brasiliensis.
```

```
XX
PN   WO2003037921-A1.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-AU001473.
XX
PR   30-OCT-2001; 2001AU-00008490.
XX
PA   (REAS-) COOP RES CENT ASTHMA.
XX
PI   O'hehir R;
XX
DR   WPI; 2003-430499/40.
XX
PT   New peptides that interact immunologically with T cells in subjects,
PT   useful for manufacturing a medicament for treating a condition associated
PT   with an aberrant, unwanted or inappropriate immune response to Hev b 6,
PT   e.g. latex allergy.
XX
PS   Example 1; Page 111; 116pp; English.
XX
CC   The invention relates to peptides that interact immunologically with T
CC   cells in subjects having latex allergy particularly to Hev b 6 allergy.
CC   Peptides and/or antibodies of the invention are useful for manufacturing
CC   a medicament for treating conditions associated with an aberrant,
CC   unwanted or inappropriate immune response to Hev b 6 or its functional
CC   homologue e.g. latex hypersensitivity or sensitivity to fruits,
CC   vegetables and/or nuts that contain class 1 chitinases. Peptides are also
CC   useful for diagnosing, monitoring, treating or preventing latex allergy
CC   or plant hypersensitivity in a subject. The present sequence is Hevea
CC   brasiliensis (rubber plant) Hev b 6 peptide
XX
SQ   Sequence 20 AA;

  Query Match             28.4%;  Score 29;  DB 6;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFE 11
              ::  :|||:|
Db          4 QLDTDGKGYE 13


RESULT 12
ADH47596
ID   ADH47596 standard; peptide; 20 AA.
XX
AC   ADH47596;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human lung tumour clone peptide, SEQ ID No 2077.
XX
KW   lung cancer; tumour; cytostatic; immunostimulant; vaccine; gene therapy;
KW   human; clone.
XX
OS   Homo sapiens.
XX
PN   WO2003037267-A2.
XX
PD   08-MAY-2003.
XX
PF   28-OCT-2002; 2002WO-US034777.
XX
PR   29-OCT-2001; 2001US-00017754.
PR   28-MAR-2002; 2002US-00113872.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Henderson RA,  Wang T,  Watanabe Y,  Kalos MD,  Sleath PR;
PI   Johnson JC,  Retter MW,  Durham M,  Carter D,  Fanger GR,  Vedvick TS;
PI   Bangur CS,  Mcnabb A;
XX
DR   WPI; 2003-468346/44.
XX
PT   New polypeptides and encoding polynucleotides, useful for diagnosing,
PT   preventing and/or treating lung cancer.
XX
PS   Example 38; SEQ ID NO 2077; 258pp; English.
XX
CC   The invention relates to novel compositions and methods for the therapy
CC   and diagnosis of cancer, particularly lung cancer. The compositions
CC   comprise one or more lung tumour polypeptides, immunogenic portions
CC   therof, polynucleotides that encode such polypeptides, antigen presenting
CC   cells that express such polypeptides, and T cells that are specific for
CC   cells expressing such polypeptides. The novel compositions have
CC   cytostatic and immunostimulant activity. The lung tumour antigens can be
CC   used in the creation of a vaccine. The polynucleotides that encode the
CC   lung tumour polypeptides can be used in gene therapy to help in the
CC   treatment of lung tumours. This sequence represents a human lung tumour
CC   clone polypeptide of the invention. This sequence was not shown in the
CC   specification. It has been taken from a World Intellectual Property
CC   Organization CD ROM supplied with the specification.
XX
SQ   Sequence 20 AA;

  Query Match             28.4%;  Score 29;  DB 7;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    6;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              || |  |   :| |:
Db          3 EGAGCSPDAPSLSGR 17


RESULT 13
ADJ21515
ID   ADJ21515 standard; peptide; 20 AA.
XX
AC   ADJ21515;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human lung cancer-related L978P peptide fragment - SEQ ID 2077.
XX
KW   lung tumour; cytostatic; lung cancer; human; L978P.
XX
OS   Homo sapiens.
XX
PN   US2003211510-A1.
XX
PD   13-NOV-2003.
XX
PF   28-OCT-2002; 2002US-00283017.
XX
PR   30-JUN-1999;   99US-00346492.
PR   15-OCT-1999;   99US-00419356.
PR   17-DEC-1999;   99US-00466867.
PR   30-DEC-1999;   99US-00476300.
PR   06-MAR-2000; 2000US-00519642.
PR   22-MAR-2000; 2000US-00533077.
PR   10-APR-2000; 2000US-00546259.
PR   27-APR-2000; 2000US-00560406.
PR   05-JUN-2000; 2000US-00589184.
PR   11-JUL-2000; 2000US-00614124.
PR   29-AUG-2000; 2000US-00651563.
PR   08-SEP-2000; 2000US-00658824.
PR   26-SEP-2000; 2000US-00671325.
PR   06-OCT-2000; 2000US-00677419.
PR   30-OCT-2000; 2000US-00702705.
PR   13-DEC-2000; 2000US-00736457.
PR   03-MAY-2001; 2001US-00849626.
PR   10-JUL-2001; 2001US-00902941.
PR   29-OCT-2001; 2001US-00017754.
PR   28-MAR-2002; 2002US-00113872.
```

```
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Henderson RA,  Wang T,  Watanabe Y,  Kalos MD,  Sleath PR;
PI   Johnson JC,  Retter MW,  Durham M,  Carter D,  Fanger GR,  Vedvick TS;
PI   Bangur CS,  Mcnabb A;
XX
DR   WPI; 2004-167010/16.
XX
PT   Novel polynucleotide encoding lung tumor polypeptides, useful for
PT   diagnosing, preventing and treating cancer e.g. lung cancer.
XX
PS   Example 37; SEQ ID NO 2077; 99pp; English.
XX
CC   The invention relates to a novel isolated polynucleotide comprising a
CC   sequence chosen from any one of 40 lung tumour polypeptides or its
CC   complements, fragments or degenerate variants. The method of the
CC   invention has cytostatic applications and may be useful for detecting and
CC   treating lung cancer in a patient, as well as for inhibiting the
CC   development of lung cancer in a patient via incubating CD4+ and/or CD8+ T
CC   cells isolated from a patient with at least one component chosen from a
CC   polypeptide, polynucleotide or antigen presenting cell (APC) of the
CC   invention and administering an effective amount of the proliferated T
CC   cells to the patient. The current sequence is that of the human lung
CC   cancer-related peptide of the invention. The current sequence is not
CC   shown in the specification per se but is available on the USPTO web-site
CC   http:seqdata.uspto.gov/sequence.html?DocID=20030211510.
XX
SQ   Sequence 20 AA;

  Query Match             28.4%;  Score 29;  DB 8;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+03;
  Matches    6;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              || |  |   :| |:
Db          3 EGAGCSPDAPSLSGR 17


RESULT 14
AAY72709
ID   AAY72709 standard; peptide; 20 AA.
XX
AC   AAY72709;
XX
DT   06-AUG-2003  (revised)
DT   31-MAY-2001  (first entry)
XX
DE   Parvovirus non-structure protein 1 (NS1) variant (T463A) peptide.
XX
KW   NS1; non-structure protein 1; cytostatic; gene therapy; toxin; therapy;
KW   tumoural disease; gene therapy; mutant; mutein; variant.
XX
OS   Parvovirus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 3
FT                   /note= "Wild type Thr substituted with Ala; This location
FT                   corresponds to position 463 of the NS1 variant (T463A)
FT                   shown in AAY72710"
XX
PN   EP1077260-A1.
XX
PD   21-FEB-2001.
XX
PF   13-AUG-1999;   99EP-00115161.
XX
PR   13-AUG-1999;   99EP-00115161.
XX
PA   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI   Nueesch J,  Rommelaere J;
XX
DR   WPI; 2001-212717/22.
DR   N-PSDB; AAD02804.
XX
PT   Novel parvovirus non-structure protein variant, useful for treating
PT   tumoral diseases, has a shifted equilibrium between DNA replication and
PT   transcription activities, and cytotoxic activity.
XX
PS   Disclosure; Page 30; 41pp; English.
XX
CC   The present sequence is a peptide fragment of parvovirus non-structure
CC   protein 1 (NS1) variant (T463A). The invention relates to the variants of
CC   the parvovirus non-structure protein (NS1) having a shifted equilibrium
CC   between the DNA replication and transcription activities, and the
CC   cytotoxicity activity. These variants are useful as toxins for treating
CC   tumoural diseases. The variant DNAs are useful as vectors for gene
CC   therapy. (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 20 AA;

  Query Match             27.9%;  Score 28.5;  DB 4;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 2.1e+03;
  Matches    8;  Conservative    1;  Mismatches    4;  Indels    3;  Gaps    1;

Qy          1 IEIGLEGKG---FEPT 13
              | |  :|||    |||
Db          4 IRIDQKGKGSKQIEPT 19


RESULT 15
AAW34804
ID   AAW34804 standard; protein; 20 AA.
XX
AC   AAW34804;
XX
DT   03-JUN-1998  (first entry)
XX
DE   Arg-specific gingipain protease derived peptide #7.
XX
KW   Arg-specific gingipain protease; gingivalis; periodontal disease;
KW   vaccine; infection.
XX
OS   Porphyromonas gingivalis.
OS   Synthetic.
XX
PN   WO9734629-A1.
XX
PD   25-SEP-1997.
XX
PF   21-MAR-1997;   97WO-US004635.
XX
PR   22-MAR-1996;   96US-0013945P.
XX
PA   (UYGE-) UNIV GEORGIA RES FOUND INC.
PA   (MORE-) MOREHOUSE SCHOOL MEDICINE.
XX
PI   Potempa J,  Travis J,  Genco C;
XX
DR   WPI; 1997-479993/44.
XX
PT   Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
PT   useful for protecting animals and humans from gingivalis and periodontal
PT   diseases.
XX
PS   Claim 1; Page 45; 95pp; English.
XX
CC   The following peptides (AAW34798-809 and AAW34810) are derived from Arg-
CC   and Lys-specific high molecular weight proteases from Porphyromonas
CC   gingivalis: YTYTVYRDGK IKEGLTATTE DDGVATGNHE YCVEKYTAGS VSPKVC (I);
CC   YTPVEEKQNG RMIVIVAKKY (II); QLPFIFDVAC VNGDFLFSMP CFAEALMRAQ (III);
CC   GEPNPYQPVS NLTATTQGQK VTLKWDAPSTK (IV); GNHEYCVEVK YTAGVSPKVC KDVTV (V);
CC   RMFMNYEPGR YTPVEEKQNG (VI); TFAGFEDTYK RMFMNYEPGR (VII); DYTYTVYRDG
CC   TKIKEGLTAT TFEEDGVATG NMEYCVCVKY TAGVSPKVC (VIII); YTYTVYRDGT KIKEGLTATTF
```

CC EEDG (IX); RDGTKIKEGL TATTFEEDGV ATGN (X); KIKEGLTATT FEEDGVATGN HEY (XI)
CC ; KWDAPNGTPN PNPN PNPNPN PGTTTLSE (XII); and YTPVEEKENG RMIVIVAKKY
CC (XIII). They are used in vaccines to protect animals, including humans,
CC from gingivitis and/or periodontal diseases
XX
SQ Sequence 20 AA;

Query Match 27.5%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          9 GFEPTLEALF 18
              ||| | : :|
Db          4 GFEDTYKRMF 13
```

Search completed: March 21, 2006, 19:14:40
Job time : 184 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:14:59 ; Search time 38 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 450

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	23.5	20	2	A61570	gamma-crystallin (
2	24	23.5	20	2	S19616	globin - polychaet
3	23	22.5	20	2	C61570	gamma-crystallin (
4	23	22.5	20	2	S78760	ribosomal protein
5	23	22.5	20	2	C49753	hypothetical prote
6	22	21.6	20	2	B61570	gamma-crystallin (
7	22	21.6	20	2	B30208	hypothetical prote
8	22	21.6	20	2	T01691	hypothetical prote
9	22	21.6	20	2	A60295	apolipophorin III
10	22	21.6	20	2	A20569	C-reactive protein
11	21	20.6	20	2	I46652	T-cell receptor de
12	21	20.6	20	2	S60668	hypothetical prote
13	21	20.6	20	2	S05411	carboxylesterase (
14	21	20.6	20	2	A35857	arginine-tRNA liga
15	21	20.6	20	2	B60505	hemoglobin A1-2 be
16	20	19.6	20	2	S04621	gamma-crystallin I
17	20	19.6	20	2	A46453	e antigen p17e pre
18	20	19.6	20	2	A60372	pollen allergen Po
19	20	19.6	20	2	A54042	mannose-6-phosphat
20	20	19.6	20	2	S38294	32K allergen - com
21	20	19.6	20	2	S38291	30K allergen - vel
22	20	19.6	20	2	A05310	apolipoprotein E -
23	19	18.6	20	2	S06466	T-cell receptor al
24	19	18.6	20	2	A45806	T-cell receptor be
25	19	18.6	20	2	S68620	histone H4 - sea u
26	19	18.6	20	2	A05332	serum amyloid P-co
27	19	18.6	20	2	S16362	opacity protein P.
28	19	18.6	20	2	A60802	25K acrosomal auto
29	18	17.6	20	2	JA0142	proteinase inhibit
30	18	17.6	20	2	C60894	gamma crystallin I
31	18	17.6	20	2	D60894	gamma crystallin V
32	18	17.6	20	2	A54519	tubulin alpha chai
33	18	17.6	20	2	PL0145	carbon-monoxide de
34	18	17.6	20	2	S57286	translation elonga
35	18	17.6	20	2	F24417	interphotoreceptor
36	18	17.6	20	2	A54538	39k major outer me
37	18	17.6	20	2	S48746	beta tubulin b-bet
38	18	17.6	20	2	A42267	J-kappa recombinat
39	18	17.6	20	2	A39543	collagen alpha 1(I
40	17	16.7	20	2	A26380	cytochrome P450 4A
41	17	16.7	20	2	A14344	alanine transamina
42	17	16.7	20	2	I46940	6-phosphofructo-2-
43	17	16.7	20	2	S09025	carboxylesterase (
44	17	16.7	20	2	S09023	carboxylesterase (
45	17	16.7	20	2	S09022	carboxylesterase (

ALIGNMENTS

RESULT 1
A61570
gamma-crystallin (total) - siamang (fragment)
C;Species: Hylobates syndactylus (siamang)
C;Date: 25-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A61570
R;Chiou, S.H.; Chang, W.P.; Ting, L.M.; Lai, T.A.; Lin, H.K.
Curr. Eye Res. 7, 1017-1022, 1988
A;Title: Biochemical characterization of lens crystallins from three mammalian species.
A;Reference number: A61570; MUID:89152306; PMID:3229121
A;Accession: A61570
A;Molecule type: protein
A;Residues: 1-20 <CHI>
A;Cross-references: UNIPROT:Q7M2W5; UNIPARC:UPI00001774A0
A;Note: 8-Glu, 9-Gln, 10-Ala, 15-Ser, 18-Thr, and 20-Ser were also found
A;Note: this preparation appears to represent the product of several gamma crystallin ge
C;Superfamily: beta-crystallin
C;Keywords: duplication; eye lens

Query Match 23.5%; Score 24; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 GLEGKGFEPT 13
              | :|: :| |
Db         10 GFQGRHYECT 19
```

RESULT 2
S19616
globin - polychaete (Eudistylia vancouveri) (fragment)
N;Alternate names: chlorocruorin
C;Species: Eudistylia vancouveri
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
C;Accession: S19616
R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H
J. Mol. Biol. 222, 1109-1129, 1991
A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular ch
A;Reference number: S19532; MUID:92106333; PMID:1762147
A;Accession: S19616
A;Molecule type: protein
A;Residues: 1-20 <QAB>
A;Cross-references: UNIPARC:UPI000017BD6D
C;Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodeca
C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match 23.5%; Score 24; DB 2; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          7 GKGFEPTLEALFG 19
              |:||   |  : |
```

```
Db          5 GRGFSYALARIDG 17


RESULT 3
C61570
gamma-crystallin (total) - European marmot (fragment)
C;Species: Marmota marmota (European marmot)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: C61570
R;Chiou, S.H.; Chang, W.P.; Ting, L.M.; Lai, T.A.; Lin, H.K.
Curr. Eye Res. 7, 1017-1022, 1988
A;Title: Biochemical characterization of lens crystallins from three mammalian species.
A;Reference number: A61570; MUID:89152306; PMID:3229121
A;Accession: C61570
A;Molecule type: protein
A;Residues: 1-20 <CHI>
A;Cross-references: UNIPROT:Q7M096; UNIPARC:UPI000017749D
A;Note: 3-Val, 6-Phe, 8-Asp, 15-His, 16-Phe, and 20-Thr were also found
A;Note: this preparation appears to represent the product of several gamma crystallin ge
C;Superfamily: beta-crystallin
C;Keywords: duplication; eye lens

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 3.4e+03;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFE 11
              | | :|: :|
Db          8 ERGFQGRCYE 17


RESULT 4
S78760
ribosomal protein MRP-L4, mitochondrial - bovine (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78760
R;Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Accession: S78760
A;Molecule type: protein
A;Residues: 1-11;12-20 <GRA>
A;Cross-references: UNIPARC:UPI000017C565; UNIPARC:UPI000017C566
C;Keywords: mitochondrion

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   38.5%;  Pred. No. 3.4e+03;
  Matches    5;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 GKGFEPTLEALFG 19
              |  | | |   :|
Db          5 GATFVPRLAEYYG 17


RESULT 5
C49753
hypothetical protein (proB 5' region) - Serratia marcescens (fragment)
C;Species: Serratia marcescens
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: C49753; S11643
R;Omori, K.; Suzuki, S.I.; Imai, Y.; Komatsubara, S.
J. Gen. Microbiol. 137, 509-517, 1991
A;Title: Analysis of the Serratia marcescens proBA operon and feedback control of prolin
A;Reference number: A49753; MUID:91237315; PMID:1851803
A;Accession: C49753
A;Molecule type: DNA
A;Residues: 1-20 <OMO>
A;Cross-references: UNIPROT:P22581; UNIPARC:UPI000013BE21; GB:X53086; NID:g47251; PIDN:C

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 3.4e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLE 6
              :|:|||
Db          1 MELGLE 6


RESULT 6
B61570
gamma-crystallin (total) - Formosa sika deer (fragment)
C;Species: Cervus nippon taiouanus (Formosa sika deer)
C;Date: 25-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: B61570
R;Chiou, S.H.; Chang, W.P.; Ting, L.M.; Lai, T.A.; Lin, H.K.
Curr. Eye Res. 7, 1017-1022, 1988
A;Title: Biochemical characterization of lens crystallins from three mammalian species.
A;Reference number: A61570; MUID:89152306; PMID:3229121
A;Accession: B61570
A;Molecule type: protein
A;Residues: 1-20 <CHI>
A;Cross-references: UNIPROT:Q7M2W4; UNIPARC:UPI00001774A1
A;Note: 6-Phe, 14-His, and 15-Cys were also found
A;Note: this preparation appears to represent the product of several gamma crystallin ge
C;Superfamily: beta-crystallin
C;Keywords: duplication; eye lens

  Query Match             21.6%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity   37.5%;  Pred. No. 4.8e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GLEGKGFE 11
              | :|: :|
Db         10 GFQGRHYE 17


RESULT 7
B30208
hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: B30208
R;Paluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988
A;Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protein s
A;Reference number: A30208; MUID:88234499; PMID:2967496
A;Accession: B30208
A;Molecule type: DNA
A;Residues: 1-20 <PAL>
A;Cross-references: UNIPARC:UPI000017B43E; GB:J03262

  Query Match             21.6%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 4.8e+03;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         10 FEPTLEALFG 19
              |  :||  ||
Db          7 FPRSLEPKFG 16


RESULT 8
T01691
hypothetical protein - maize chloroplast (fragment)
C;Species: chloroplast Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01691
R;Werr, W.
submitted to the EMBL Data Library, June 1982
A;Reference number: Z14397
A;Accession: T01691
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-20 <WER>
A;Cross-references: UNIPROT:Q33294; UNIPARC:UPI000008E44A; EMBL:V01469; NID:g14307; PIDN
C;Genetics:
```

```
A;Genome: chloroplast
A;Note: Intron positions not resolved (incomplete sequence)
C;Keywords: chloroplast

  Query Match             21.6%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEAL 17
              |||||
Db         13 TLEAL 17


RESULT 9
A60295
apolipophorin III - house cricket (fragment)
C;Species: Acheta domesticus (house cricket)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
C;Accession: A60295
R;Strobel, L.M.; Kanost, M.R.; Ziegler, R.; Wells, M.A.
Insect Biochem. 20, 859-863, 1990
A;Title: Adipokinetic hormone causes formation of a low density lipophorin in the house
A;Reference number: A60295
A;Accession: A60295
A;Molecule type: protein
A;Residues: 1-20 <STR>
A;Cross-references: UNIPROT:Q7M484; UNIPARC:UPI000017BE16
C;Comment: This protein, a small, water-soluble apolipoprotein, is thought to increase t
ts a residual pathway for flight-related lipid transport.
C;Keywords: hemolymph; lipid transport

  Query Match             21.6%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity   33.3%;  Pred. No. 4.8e+03;
  Matches    5;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEA 16
              : |  |  |    ||
Db          1 DAGTTGADFNSLFEA 15


RESULT 10
A20569
C-reactive protein - smooth dogfish (fragment)
C;Species: Mustelus canis (smooth dogfish)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: A20569
R;Robey, F.A.; Tanaka, T.; Liu, T.Y.
J. Biol. Chem. 258, 3889-3894, 1983
A;Title: Isolation and characterization of two major serum proteins from the dogfish, Mu
A;Reference number: A92419; MUID:83160932; PMID:6403520
A;Accession: A20569
A;Molecule type: protein
A;Residues: 1-20 <ROB>
A;Cross-references: UNIPROT:P19094; UNIPARC:UPI000012847A

  Query Match             21.6%;  Score 22;  DB 2;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 4.8e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GLEGKGFE 11
              || ||  :
Db         12 GLAGKALD 19


RESULT 11
I46652
T-cell receptor delta-chain J-delta-1 segment - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46652
R;Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A;Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A;Reference number: I46623; MUID:95363165; PMID:7636249
A;Accession: I46652
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-20 <YAN>
A;Cross-references: UNIPARC:UPI000011B2B7; GB:D49560; NID:g1041172; PIDN:BAA08504.1; PID
C;Keywords: T-cell receptor

  Query Match             20.6%;  Score 21;  DB 2;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 7e+03;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 EPTLEALFGK 20
              : | : :|||
Db          3 DDTDKLIFGK 12


RESULT 12
S60668
hypothetical protein 3 - Klebsiella pneumoniae (fragment)
C;Species: Klebsiella pneumoniae
C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 09-Jul-2004
C;Accession: S60668
R;Merrick, M.J.; Taylor, M.
submitted to the EMBL Data Library, August 1995
A;Description: Sequence and characterisation of distal genes in the Klebsiella pneumonia
A;Reference number: S60666
A;Accession: S60668
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-20 <MER>
A;Cross-references: UNIPROT:Q48474; UNIPARC:UPI00000B751C; EMBL:Z50803; NID:g950054; PI

  Query Match             20.6%;  Score 21;  DB 2;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 7e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 LEGKGF 10
              | |:||
Db          8 LGGEGF 13


RESULT 13
S05411
carboxylesterase (EC 3.1.1.1) - Sulfolobus acidocaldarius (fragment)
N;Alternate names: serine esterase
C;Species: Sulfolobus acidocaldarius
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S05411
R;Sobek, H.; Goerisch, H.
Biochem. J. 261, 993-998, 1989
A;Title: Further kinetic and molecular characterization of an extremely heat-stable car
A;Reference number: S05411; MUID:90026296; PMID:2508625
A;Accession: S05411
A;Molecule type: protein
A;Residues: 1-20 <SOB>
A;Cross-references: UNIPROT:Q7M529; UNIPARC:UPI000017AEB3
A;Note: 1-Ala and 1-Ser were also found
C;Keywords: carboxylic ester hydrolase; tetramer

  Query Match             20.6%;  Score 21;  DB 2;  Length 20;
  Best Local Similarity   42.9%;  Pred. No. 7e+03;
  Matches    3;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 EPTLEAL 17
              :||:: |
Db          3 DPTIKCL 9


RESULT 14
A35857
arginine-tRNA ligase (EC 6.1.1.19) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
```

C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35857
R;Sivaram, P.; Deutscher, M.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 3665-3669, 1990
A;Title: Existence of two forms of rat liver arginyl-tRNA synthetase suggests channeling
A;Reference number: A35857; MUID:90251617; PMID:2187187
A;Accession: A35857
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <SIV>
A;Cross-references: UNIPROT:P40329; UNIPARC:UPI000013665D
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

  Query Match 20.6%; Score 21; DB 2; Length 20;
  Best Local Similarity 66.7%; Pred. No. 7e+03;
  Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 14 LEALFG 19
  |: |||
Db 8 LQELFG 13

RESULT 15
B60505
hemoglobin A1-2 beta chain [validated] - sockeye salmon (fragment)
C;Species: Oncorhynchus nerka (sockeye salmon)
C;Date: 19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change 09-Jul-2004
C;Accession: B60505
R;Duffy, L.K.; Reynolds, R.; Harrington, J.P.
Comp. Biochem. Physiol. B 96, 41-45, 1990
A;Title: Partial amino acid sequences of several globin chains from the sockeye salmon,
A;Reference number: A60505; MUID:90305433; PMID:2364674
A;Accession: B60505
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <DUF>
A;Cross-references: UNIPROT:Q7LZL8; UNIPARC:UPI0000177118
C;Keywords: blood; oxygen carrier

  Query Match 20.6%; Score 21; DB 2; Length 20;
  Best Local Similarity 66.7%; Pred. No. 7e+03;
  Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IGLEGK 8
  :|| ||
Db 12 VGLWGK 17

Search completed: March 21, 2006, 19:19:17
Job time : 40 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:11:43 ; Search time 227 Seconds
(without alignments)
62.161 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 1900

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	28.4	20	2	Q6UVM6_9FLAV	Q6uvm6 gb virus c/
2	26	25.5	20	1	PORC_METTM	P80902 methanobact
3	25	24.5	20	2	Q9UWH0_9EURY	Q9uwh0 thermococcu
4	25	24.5	20	2	Q9R4I4_DESGI	Q9r4i4 desulfovibr
5	24	23.5	20	2	Q7M2W5_HYLSY	Q7m2w5 hylobates s
6	23	22.5	20	1	TPX_CLOPA	P81361 clostridium
7	23	22.5	20	1	YPRB_SERMA	P22581 serratia ma
8	23	22.5	20	2	Q7RRY4_PLAYO	Q7rry4 plasmodium
9	23	22.5	20	2	Q5K4V0_BOVIN	Q5k4v0 bos taurus
10	23	22.5	20	2	Q865L1_PIG	Q865l1 sus scrofa
11	23	22.5	20	2	Q9S8Y1_POPTM	Q9s8y1 populus tre
12	23	22.5	20	2	Q7M096_MARMR	Q7m096 marmota mar
13	23	22.5	20	2	Q993N6_9HIV1	Q993n6 human immun
14	23	22.5	20	2	Q993N8_9HIV1	Q993n8 human immun
15	23	22.5	20	2	Q993P2_9HIV1	Q993p2 human immun
16	23	22.5	20	2	Q993P4_9HIV1	Q993p4 human immun
17	23	22.5	20	2	Q993P8_9HIV1	Q993p8 human immun
18	23	22.5	20	2	Q993Q0_9HIV1	Q993q0 human immun
19	23	22.5	20	2	Q993Q4_9HIV1	Q993q4 human immun
20	23	22.5	20	2	Q993Q6_9HIV1	Q993q6 human immun
21	23	22.5	20	2	Q993R0_9HIV1	Q993r0 human immun
22	23	22.5	20	2	Q993R2_9HIV1	Q993r2 human immun
23	23	22.5	20	2	Q993R6_9HIV1	Q993r6 human immun
24	23	22.5	20	2	Q993R8_9HIV1	Q993r8 human immun
25	22	21.6	20	1	CRP_MUSCA	P19094 mustelus ca
26	22	21.6	20	1	DERP6_DERPT	P49277 dermatophag
27	22	21.6	20	2	Q7M484_ACHDO	Q7m484 acheta dome
28	22	21.6	20	2	Q7YSG8_DROME	Q7ysg8 drosophila
29	22	21.6	20	2	Q9TWR0_BLAGE	Q9twr0 blattella g
30	22	21.6	20	2	Q9U8M6_9DIPT	Q9u8m6 liodrosophi
31	22	21.6	20	2	Q7M2W4_CERNT	Q7m2w4 cervus nipp
32	22	21.6	20	2	Q33294_MAIZE	Q33294 zea mays (m
33	22	21.6	20	2	Q9S8C3_LUPAL	Q9s8c3 lupinus alb
34	22	21.6	20	2	P83078_BACCE	P83078 bacillus ce
35	22	21.6	20	2	Q9R731_XANCA	Q9r731 xanthomonas
36	22	21.6	20	2	Q62435_MOUSE	Q62435 mus musculu
37	22	21.6	20	2	Q8JJ13_CARAU	Q8jj13 carassius a
38	22	21.6	20	2	Q9PWQ4_CHICK	Q9pwq4 gallus gall
39	22	21.6	20	2	Q7SM57_9DELA	Q7sm57 human t-lym
40	22	21.6	20	2	Q7SM59_9DELA	Q7sm59 human t-lym
41	22	21.6	20	2	Q8Q2S6_9DELA	Q8q2s6 human t-lym
42	22	21.6	20	2	Q8Q2S7_9DELA	Q8q2s7 human t-lym
43	22	21.6	20	2	Q8Q2S8_9DELA	Q8q2s8 human t-lym
44	22	21.6	20	2	Q8Q2S9_9DELA	Q8q2s9 human t-lym
45	21	20.6	20	1	SYR_RAT	P40329 rattus norv

ALIGNMENTS

RESULT 1
Q6UVM6_9FLAV
ID Q6UVM6_9FLAV PRELIMINARY; PRT; 20 AA.
AC Q6UVM6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P187 (Fragment).
OS GB virus C/Hepatitis G virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC GBV-C/HGV group.
OX NCBI_TaxID=54290;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jordan E.L., Souza I., McLinden J.H., Murthy K., Xiang J.,
RA Stapleton J.T.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY359288; AAR11302.1; -; Genomic_RNA.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2207 MW; 3D374493CD9BDEC5 CRC64;

Query Match 28.4%; Score 29; DB 2; Length 20;
Best Local Similarity 54.5%; Pred. No. 3.7e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 IGLEGKGFEPT 13
              ||| |   :||
Db          7 IGLSGVNRDPT 17
```

RESULT 2
PORC_METTM
ID PORC_METTM STANDARD; PRT; 20 AA.
AC P80902;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Pyruvate synthase subunit PORC (EC 1.2.7.1) (Pyruvate oxidoreductase
DE gamma chain) (POR) (Pyruvic-ferredoxin oxidoreductase gamma subunit)
DE (Fragment).
GN Name=porC;
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.

```
CC   -!- COFACTOR: Binds 2 4Fe-4S clusters (By similarity).
CC   -!- BIOPHYSICOCHEMICAL PROPERTIES:
CC       pH dependence:
CC         Optimum pH is 10.0;
CC       Temperature dependence:
CC         Optimum temperature is 80 degrees Celsius;
CC   -!- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC       gamma chain.
CC   -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
KW   4Fe-4S; Direct protein sequencing; Electron transport; Iron;
KW   Iron-sulfur; Metal-binding; Oxidoreductase; Repeat; Transport.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2168 MW;  481532134D42F353 CRC64;

  Query Match             25.5%;  Score 26;  DB 1;  Length 20;
  Best Local Similarity   37.5%;  Pred. No. 1.1e+04;
  Matches    6;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEA 16
              |||   |:| :  : |
Db          2 IEIRFHGRGGQXAVTA 17


RESULT 3
Q9UWH0_9EURY
ID   Q9UWH0_9EURY PRELIMINARY;      PRT;    20 AA.
AC   Q9UWH0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Keto-valine-ferredoxin oxidoreductase gamma-subunit, VOR gamma
DE   (Fragment).
OS   Thermococcus sp.
OC   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC   Thermococcus.
OX   NCBI_TaxID=35749;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   STRAIN=ES-1;
RX   MEDLINE=96146528; PubMed=8550513;
RA   Heider J., Mai X., Adams M.W.;
RT   "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
RT   new and reversible coenzyme A-dependent enzyme involved in peptide
RT   fermentation by hyperthermophilic archaea.";
RL   J. Bacteriol. 178:780-787(1996).
SQ   SEQUENCE   20 AA;  2010 MW;  9D76B21E2022F341 CRC64;

  Query Match             24.5%;  Score 25;  DB 2;  Length 20;
  Best Local Similarity   31.2%;  Pred. No. 1.6e+04;
  Matches    5;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEA 16
              ||:   |:| :  : |
Db          2 IEVRFHGRGGQGAVTA 17


RESULT 4
Q9R4I4_DESGI
ID   Q9R4I4_DESGI  PRELIMINARY;      PRT;    20 AA.
AC   Q9R4I4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   BENZYLVIOLOGEN-linked aldehyde oxidoreductase (Fragment).
OS   Desulfovibrio gigas.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC   Desulfovibrionaceae; Desulfovibrio.
OX   NCBI_TaxID=879;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=96042096; PubMed=7592385;
RA   Hensgens C.M., Hagen W.R., Hansen T.A.;
RT   "Purification and characterization of a benzylviologen-linked,
RT   tungsten-containing aldehyde oxidoreductase from Desulfovibrio
RT   gigas.";
RL   J. Bacteriol. 177:6195-6200(1995).
SQ   SEQUENCE   20 AA;  2128 MW;  1A9608A1881902BC CRC64;

  Query Match             24.5%;  Score 25;  DB 2;  Length 20;
  Best Local Similarity   57.1%;  Pred. No. 1.6e+04;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IEIGLEG 7
              |::| ||
Db          7 IDVGAEG 13


RESULT 5
Q7M2W5_HYLSY
ID   Q7M2W5_HYLSY PRELIMINARY;      PRT;    20 AA.
AC   Q7M2W5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Gamma-crystallin (total) (Fragment).
OS   Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Hylobatidae; Symphalangus.
OX   NCBI_TaxID=9590;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=89152306; PubMed=3229121;
RA   Chiou S.H., Chang W.P., Ting L.M., Lai T.A., Lin H.K.;
RT   "Biochemical characterization of lens crystallins from three mammalian
RT   species.";
RL   Curr. Eye Res. 7:1017-1022(1988).
DR   PIR; A61570; A61570.
DR   HSSP; P02528; 1A5D.
DR   InterPro; IPR001064; Crystallin.
DR   Pfam; PF00030; Crystall; 1.
DR   PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 1.
FT   NON_TER       1      1
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2409 MW;  E5ED418E0900AB23 CRC64;

  Query Match             23.5%;  Score 24;  DB 2;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 2.3e+04;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GLEGKGFEPT 13
              | :|: :| |
Db         10 GFQGRHYECT 19


RESULT 6
TPX_CLOPA
ID   TPX_CLOPA      STANDARD;      PRT;    20 AA.
AC   P81361;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Probable thiol peroxidase (EC 1.11.1.-) (CP 42) (Fragment).
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   PROTEIN SEQUENCE.
```

```
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- FUNCTION: Has antioxidant activity. Could remove peroxides or
CC       H(2)O(2) (By similarity).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:
CC       4.6, its MW is: 20.2 kDa.
CC   -!- SIMILARITY: Belongs to the ahpC/TSA family. Tpx subfamily.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   HAMAP; MF_00269; -; 1.
DR   InterPro; IPR002065; TPX.
DR   PROSITE; PS01265; TPX; PARTIAL.
KW   Antioxidant; Direct protein sequencing; Oxidoreductase; Peroxidase.
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2193 MW;  08178FCD2782E765 CRC64;

  Query Match             22.5%;  Score 23;  DB 1;  Length 20;
  Best Local Similarity   57.1%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 EIGLEGK 8
              |: |:||
Db          9 EVTLQGK 15


RESULT 7
YPRB_SERMA
ID   YPRB_SERMA     STANDARD;      PRT;    20 AA.
AC   P22581;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Hypothetical protein in proB 5'region (Fragment).
OS   Serratia marcescens.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Serratia.
OX   NCBI_TaxID=615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   STRAIN=Sr41;
RX   MEDLINE=91237315; PubMed=1851803;
RA   Omori K., Suzuki S., Imai Y., Komatsubara S.;
RT   "Analysis of the Serratia marcescens proBA operon and feedback control
RT   of proline biosynthesis.";
RL   J. Gen. Microbiol. 137:509-517(1991).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; D90351; BAA14363.1; -; Genomic_DNA.
DR   EMBL; X53086; CAA37253.1; -; Genomic_DNA.
DR   PIR; C49753; C49753.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   20 AA;  2248 MW;  4DD7777735276674 CRC64;

  Query Match             22.5%;  Score 23;  DB 1;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLE 6
                :|:|||
Db          1 MELGLE 6


RESULT 8
Q7RRY4_PLAYO
ID   Q7RRY4_PLAYO PRELIMINARY;      PRT;    20 AA.
AC   Q7RRY4;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   Name=PY00583;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=17XNL;
RX   MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01000159; EAA17061.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER      1      1
SQ   SEQUENCE   20 AA;  2293 MW;  DEFA2E15ED32E8D4 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 3.2e+04;
  Matches    7;  Conservative    3;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          6 EGKGFE--PTLEAL 17
              :||| :   |||:|
Db          3 QGKGTKCRITLESL 16


RESULT 9
Q5K4V0_BOVIN
ID   Q5K4V0_BOVIN PRELIMINARY;      PRT;    20 AA.
AC   Q5K4V0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Zinc finger Y-chromosomal protein (Fragment).
GN   Name=zfy;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Durstewitz G., Werner F.A.O., Buitkamp J., Thaller G., Kraemer W.,
RA   Kollers S., Brem G., Pfistershammer J., Irps U., Borchers H.,
RA   Mosner J., Fries R.;
RT   "Discovery of SNPs for digital DNA signatures in cattle.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ507102; CAD45343.1; -; Genomic_DNA.
DR   GO; GO:0005634; C:nucleus; IEA.
```

```
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF00096; zf-C2H2; 1.
DR   ProDom; PD000003; Znf_C2H2; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
FT   NON_TER       1      1
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2320 MW;  931EC10F3FDDBE2F CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GKGF 10
              ||||
Db          2 GKGF 5


RESULT 10
Q865L1_PIG
ID   Q865L1_PIG  PRELIMINARY;      PRT;    20 AA.
AC   Q865L1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Myogenic factor 6 (Fragment).
GN   Name=MYF6;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=12755833; DOI=10.1046/j.1365-2052.2003.01012.x;
RA   Vykoukalova Z., Knoll A., Dvorak J., Rohrer G.A., Cepica S.;
RT   "Linkage and radiation hybrid mapping of the porcine MYF6 gene to
RT   chromosome 5.";
RL   Anim. Genet. 34:238-240(2003).
DR   EMBL; AY227664; AAO46103.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2410 MW;  936B690E8EC13210 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   28.6%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLE 15
              |:|::   : |  |
Db          6 ELGVDPFSYRPKQE 19


RESULT 11
Q9S8Y1_POPTM
ID   Q9S8Y1_POPTM  PRELIMINARY;      PRT;    20 AA.
AC   Q9S8Y1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   BISPECIFIC caffeic acid/5-HYDROXYFERULIC acid O-methyltransferase, OMT
DE   (EC 2.1.1.68) (Fragment).
OS   Populus tremuloides (Quaking aspen).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
OX   NCBI_TaxID=3693;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   PubMed=1368360; DOI=10.1016/0031-9422(92)83093-E;
RA   Bugos R.C., Chiang V.L., Campbell W.H.;
RT   "Characterization of bispecific caffeic acid/5-hydroxyferulic acid O-
RT   methyltransferase from aspen.";
RL   Phytochemistry 31:1495-1498(1992).
DR   HSSP; P28002; 1KYZ.
DR   GO; GO:0047763; F:caffeate O-methyltransferase activity; IEA.
DR   InterPro; IPR001077; O_Met_trans2.
DR   Pfam; PF00891; Methyltransf_2; 1.
SQ   SEQUENCE   20 AA;  2338 MW;  0898587DFDF1AC70 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   33.3%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALFGK 20
              | :|    :| |
Db          3 GTDPRFNKVFNK 14


RESULT 12
Q7M096_MARMR
ID   Q7M096_MARMR PRELIMINARY;      PRT;    20 AA.
AC   Q7M096;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Gamma-crystallin (total) (Fragment).
OS   Marmota marmota (Alpine marmot).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Sciuridae; Sciurinae; Marmota.
OX   NCBI_TaxID=9993;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=89152306; PubMed=3229121;
RA   Chiou S.H., Chang W.P., Ting L.M., Lai T.A., Lin H.K.;
RT   "Biochemical characterization of lens crystallins from three mammalian
RT   species.";
RL   Curr. Eye Res. 7:1017-1022(1988).
DR   PIR; C61570; C61570.
DR   HSSP; P02526; 1AMM.
DR   InterPro; IPR001064; Crystallin.
DR   Pfam; PF00030; Crystall; 1.
DR   PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 1.
FT   NON_TER       1      1
FT   NON_TER      20     20
SQ   SEQUENCE   20 AA;  2361 MW;  E1F9518E084AFB23 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFE 11
              | | :|: :|
Db          8 ERGFQGRCYE 17


RESULT 13
Q993N6_9HIV1
ID   Q993N6_9HIV1 PRELIMINARY;      PRT;    20 AA.
AC   Q993N6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Gag protein (Fragment).
GN   Name=gag;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC   Primate lentivirus group.
OX   NCBI_TaxID=11676;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21136890; PubMed=11238855;
RX   DOI=10.1128/JVI.75.7.3291-3300.2001;
RA   Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
```

```
RT   "Individual contributions of mutant protease and reverse transcriptase
RT   to viral infectivity, replication, and protein maturation of
RT   antiretroviral drug-resistant human immunodeficiency virus type 1.";
RL   J. Virol. 75:3291-3300(2001).
DR   EMBL; AF316851; AAK21104.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   20 AA;  2194 MW;  B9EBC80E8A3B1340 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   57.1%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALFG 19
              :|::|||
Db          8 SLKSLFG 14


RESULT 14
Q993N8_9HIV1
ID   Q993N8_9HIV1 PRELIMINARY;      PRT;    20 AA.
AC   Q993N8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Gag protein (Fragment).
GN   Name=gag;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC   Primate lentivirus group.
OX   NCBI_TaxID=11676;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21136890; PubMed=11238855;
RX   DOI=10.1128/JVI.75.7.3291-3300.2001;
RA   Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT   "Individual contributions of mutant protease and reverse transcriptase
RT   to viral infectivity, replication, and protein maturation of
RT   antiretroviral drug-resistant human immunodeficiency virus type 1.";
RL   J. Virol. 75:3291-3300(2001).
DR   EMBL; AF316850; AAK21102.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   20 AA;  2194 MW;  B9EBC80E8A3B1340 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   57.1%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALFG 19
              :|::|||
Db          8 SLKSLFG 14


RESULT 15
Q993P2_9HIV1
ID   Q993P2_9HIV1 PRELIMINARY;      PRT;    20 AA.
AC   Q993P2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Gag protein (Fragment).
GN   Name=gag;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC   Primate lentivirus group.
OX   NCBI_TaxID=11676;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21136890; PubMed=11238855;
RX   DOI=10.1128/JVI.75.7.3291-3300.2001;
RA   Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT   "Individual contributions of mutant protease and reverse transcriptase
RT   to viral infectivity, replication, and protein maturation of
RT   antiretroviral drug-resistant human immunodeficiency virus type 1.";
RL   J. Virol. 75:3291-3300(2001).
DR   EMBL; AF316847; AAK21098.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   20 AA;  2167 MW;  B9EBC80E8A2AE340 CRC64;

  Query Match             22.5%;  Score 23;  DB 2;  Length 20;
  Best Local Similarity   57.1%;  Pred. No. 3.2e+04;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALFG 19
              :|::|||
Db          8 SLKSLFG 14


Search completed: March 21, 2006, 19:18:33
Job time : 229 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:18:49 ; Search time 46 Seconds
(without alignments)
35.946 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 10165

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	28.5	27.9	20	2	US-10-069-056-17	Sequence 17, Appl
2	28	27.5	20	2	US-08-822-324-17	Sequence 17, Appl
3	27	26.5	20	2	US-08-256-747C-2	Sequence 2, Appli
4	27	26.5	20	2	US-08-834-130A-2	Sequence 2, Appli
5	27	26.5	20	2	US-09-962-756-1138	Sequence 1138, Ap
6	26	25.5	20	1	US-07-994-277A-4	Sequence 4, Appli
7	26	25.5	20	2	US-09-591-694-24	Sequence 24, Appl
8	26	25.5	20	2	US-09-962-756-1132	Sequence 1132, Ap
9	26	25.5	20	2	US-09-747-287A-198	Sequence 198, App
10	26	25.5	20	2	US-09-394-019C-150	Sequence 150, App
11	26	25.5	20	2	US-09-394-019C-395	Sequence 395, App
12	25	24.5	20	2	US-09-043-560B-8	Sequence 8, Appli
13	25	24.5	20	2	US-09-171-432A-52	Sequence 52, Appl
14	25	24.5	20	2	US-09-743-209A-6	Sequence 6, Appli
15	25	24.5	20	2	US-09-394-019C-123	Sequence 123, App
16	25	24.5	20	2	US-09-394-019C-124	Sequence 124, App
17	25	24.5	20	2	US-09-394-019C-239	Sequence 239, App
18	25	24.5	20	2	US-09-394-019C-257	Sequence 257, App
19	25	24.5	20	2	US-09-394-019C-368	Sequence 368, App
20	25	24.5	20	2	US-09-394-019C-369	Sequence 369, App
21	24	23.5	20	1	US-08-440-861-22	Sequence 22, Appl
22	24	23.5	20	1	US-08-484-530-35	Sequence 35, Appl
23	24	23.5	20	1	US-08-827-618A-35	Sequence 35, Appl
24	24	23.5	20	2	US-08-483-952A-35	Sequence 35, Appl
25	24	23.5	20	2	US-09-643-597-249	Sequence 249, App
26	24	23.5	20	2	US-08-476-501-35	Sequence 35, Appl
27	24	23.5	20	2	US-09-480-884A-249	Sequence 249, App
28	24	23.5	20	2	US-09-542-615A-249	Sequence 249, App
29	24	23.5	20	2	US-09-606-421B-249	Sequence 249, App
30	24	23.5	20	2	US-09-476-496A-249	Sequence 249, App
31	24	23.5	20	2	US-09-674-674D-28	Sequence 28, Appl
32	24	23.5	20	2	US-09-630-940B-249	Sequence 249, App
33	24	23.5	20	2	US-10-007-700-249	Sequence 249, App
34	24	23.5	20	2	US-10-007-700-401	Sequence 401, App
35	23	22.5	20	1	US-08-564-972-5	Sequence 5, Appli
36	23	22.5	20	1	US-08-053-451B-114	Sequence 114, App
37	23	22.5	20	2	US-08-890-157A-2	Sequence 2, Appli
38	23	22.5	20	2	US-09-027-998A-53	Sequence 53, Appl
39	23	22.5	20	2	US-09-043-560B-7	Sequence 7, Appli
40	23	22.5	20	2	US-09-790-497A-100	Sequence 100, App
41	23	22.5	20	2	US-09-428-082B-368	Sequence 368, App
42	23	22.5	20	2	US-09-674-674D-30	Sequence 30, Appl
43	23	22.5	20	2	US-08-838-128B-25	Sequence 25, Appl
44	23	22.5	20	2	US-09-962-756-27	Sequence 27, Appl
45	23	22.5	20	2	US-09-962-756-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-069-056-17
; Sequence 17, Application US/10069056
; Patent No. 6919196
; GENERAL INFORMATION:
; APPLICANT: Nuesch, Jurg
; APPLICANT: Rommelaere, Jean
; TITLE OF INVENTION: Parvovirus NS 1 Variants
; FILE REFERENCE: 4121-136
; CURRENT APPLICATION NUMBER: US/10/069,056
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: PCT/EP00/07835
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: EP 99 115 161.4
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Part of Parvovirus NS1 Variant
US-10-069-056-17

Query Match 27.9%; Score 28.5; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

```
Qy          1 IEIGLEGKG---FEPT 13
              | |  :|||    |||
Db          4 IRIDQKGKGSKQIEPT 19
```

RESULT 2
US-08-822-324-17
; Sequence 17, Application US/08822324
; Patent No. 6129917
; GENERAL INFORMATION:
; APPLICANT: Potempa, Jan S.
; APPLICANT: Travis, James
; APPLICANT: Genco, Caroline A.
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US

```
;       ZIP:  80303
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/822,324
;       FILING DATE:  21-MAR-1997
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/013,945
;       FILING DATE:  22-MAR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Ferber, Donna M.
;       REGISTRATION NUMBER:  33,878
;       REFERENCE/DOCKET NUMBER:  103-95 WO
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 488-8080
;       TELEFAX:  (303) 499-8089
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  not relevant
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
US-08-822-324-17

  Query Match             27.5%;  Score 28;  DB 2;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5.6e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALF 18
              ||| | : :|
Db          4 GFEDTYKRMF 13


RESULT 3
US-08-256-747C-2
; Sequence 2, Application US/08256747C
; Patent No. 6037448
;  GENERAL INFORMATION:
;    APPLICANT:  CHONG, Pele
;    APPLICANT:  GILLAM, Shirley
;    APPLICANT:  OU, Dawei
;    APPLICANT:  TINGLE, Aubrey
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
;    NUMBER OF SEQUENCES:  78
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6th Floor 701, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/256,747C
;      FILING DATE:  06-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Stewart, Michael I.
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-370
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-256-747C-2

  Query Match             26.5%;  Score 27;  DB 2;  Length 20;
  Best Local Similarity   45.5%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFE 11
              : : | | |||
Db          1 VPVRLAGVGFE 11


RESULT 4
US-08-834-130A-2
; Sequence 2, Application US/08834130A
; Patent No. 6180758
;  GENERAL INFORMATION:
;    APPLICANT:  CHONG, Pele
;    APPLICANT:  GILLAM, Shirley
;    APPLICANT:  OU, Dawei
;    APPLICANT:  TINGLE, Aubrey
;    TITLE OF INVENTION:  SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sim & McBurney
;      STREET:  6th Floor, 330 University Avenue
;      CITY:  Toronto
;      STATE:  Ontario
;      COUNTRY:  Canada
;      ZIP:  M5G 1R7
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/834,130A
;      FILING DATE:  14-APR-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  STEWART, Michael I
;      REGISTRATION NUMBER:  24,973
;      REFERENCE/DOCKET NUMBER:  1038-686 MIS:jb
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (416) 595-1155
;      TELEFAX:  (416) 595-1163
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-834-130A-2

  Query Match             26.5%;  Score 27;  DB 2;  Length 20;
  Best Local Similarity   45.5%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFE 11
              : : | | |||
Db          1 VPVRLAGVGFE 11


RESULT 5
US-09-962-756-1138
; Sequence 1138, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
```

```
;  APPLICANT: PILLUTLA, RENUKA
;  APPLICANT:  BRISSETTE, RENEE
;  APPLICANT:  BLUME, ARTHUR J.
;  APPLICANT:  SCHAFFER, LAUGE
;  APPLICANT:  BRANDT, JAKOB
;  APPLICANT:  GOLDSTEIN, NEIL I.
;  APPLICANT:  SPETZLER, JANE
;  APPLICANT:  OSTERGAARD, SOREN
;  APPLICANT:  HANSEN, PER HERTZ
;  TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
;  FILE REFERENCE: 1878-4051US1
;  CURRENT APPLICATION NUMBER: US/09/962,756
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 09/538,038
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: 09/146,127
;  PRIOR FILING DATE: 1998-09-02
;  NUMBER OF SEQ ID NOS: 2227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1138
;    LENGTH: 20
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: peptide
US-09-962-756-1138

  Query Match             26.5%;  Score 27;  DB 2;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 EALFGK 20
              |:||||
Db         12 ESLFGK 17


RESULT 6
US-07-994-277A-4
; Sequence 4, Application US/07994277A
; Patent No. 5536497
;  GENERAL INFORMATION:
;    APPLICANT:  Evans, Richard T.
;    APPLICANT:  Bedi, Gurrinder S.
;    APPLICANT:  Genco, Robert J.
;    APPLICANT:  Sojar, Hakimuddin T.
;    TITLE OF INVENTION:  Fimbrial Polypeptides
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hodgson, Russ, Andrews, Woods & Goodyear
;      STREET:  1800 One M&T Plaza
;      CITY:  Buffalo
;      STATE:  New York
;      COUNTRY:  United States
;      ZIP:  14203-2391
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch
;      COMPUTER:  IBM compatible/CompuAdd 325TX
;      OPERATING SYSTEM:  MS-DOS/Microsoft Windows 3.1
;      SOFTWARE:  Wordperfect for Windows 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/994,277A
;      FILING DATE:  19921221
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelson, M. Bud
;      REGISTRATION NUMBER:  35,300
;      REFERENCE/DOCKET NUMBER:  11520.0040
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 856-4000
;      TELEFAX:  (716) 849-0349
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acid residues
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  peptide
;    HYPOTHETICAL:  no
;    FRAGMENT TYPE:  internal
;    PUBLICATION INFORMATION:
;      RELEVANT RESIDUES IN SEQ ID NO:  From 226-245
;      RELEVANT RESIDUES IN SEQ ID NO:  (without counting the first 10 amino acids which
;      RELEVANT RESIDUES IN SEQ ID NO:  the leader sequence)
US-07-994-277A-4

  Query Match             25.5%;  Score 26;  DB 1;  Length 20;
  Best Local Similarity   44.4%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         12 PTLEALFGK 20
              ||:  ::||
Db          3 PTILCVYGK 11


RESULT 7
US-09-591-694-24
; Sequence 24, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
;  APPLICANT: John C. Reed
;  APPLICANT: Shu-ichi Matsuzawa
;  TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
;  TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto
;  FILE REFERENCE: P-LJ 4220
;  CURRENT APPLICATION NUMBER: US/09/591,694
;  CURRENT FILING DATE: 2000-06-09
;  EARLIER APPLICATION NUMBER: US 09/330,517
;  EARLIER FILING DATE: 1999-06-11
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;    LENGTH: 20
;    TYPE: PRT
;    ORGANISM: Homo sapien
US-09-591-694-24

  Query Match             25.5%;  Score 26;  DB 2;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGF 10
              :   | |:||
Db          9 VSAALRGRGF 18


RESULT 8
US-09-962-756-1132
; Sequence 1132, Application US/09962756
; Patent No. 6875741
; GENERAL INFORMATION:
;  APPLICANT: PILLUTLA, RENUKA
;  APPLICANT:  BRISSETTE, RENEE
;  APPLICANT:  BLUME, ARTHUR J.
;  APPLICANT:  SCHAFFER, LAUGE
;  APPLICANT:  BRANDT, JAKOB
;  APPLICANT:  GOLDSTEIN, NEIL I.
;  APPLICANT:  SPETZLER, JANE
;  APPLICANT:  OSTERGAARD, SOREN
;  APPLICANT:  HANSEN, PER HERTZ
;  TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
;  FILE REFERENCE: 1878-4051US1
;  CURRENT APPLICATION NUMBER: US/09/962,756
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: 09/538,038
;  PRIOR FILING DATE: 2000-03-29
```

```
;  PRIOR APPLICATION NUMBER: 09/146,127
;  PRIOR FILING DATE: 1998-09-02
;  NUMBER OF SEQ ID NOS: 2227
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1132
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-962-756-1132

  Query Match             25.5%;  Score 26;  DB 2;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 EALFGK 20
              |||||:
Db         12 EALFGQ 17


RESULT 9
US-09-747-287A-198
; Sequence 198, Application US/09747287A
; Patent No. 6893868
; GENERAL INFORMATION:
;  APPLICANT: KOMORIYA, AKIRA
;  APPLICANT:  PACKARD, BEVERLY S.
;  TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
;  TITLE OF INVENTION:  ACTIVITY IN BIOLOGICAL SAMPLES
;  FILE REFERENCE: 300-948600US
;  CURRENT APPLICATION NUMBER: US/09/747,287A
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/349,019
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: US08/802,981
;  PRIOR FILING DATE: 1997-02-20
;  PRIOR APPLICATION NUMBER: PCT/US00/24882
;  PRIOR FILING DATE: 2000-09-11
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 198
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: Xaa is episilon-aminocaproic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: Xaa is episilon-aminocaproic acid
US-09-747-287A-198

  Query Match             25.5%;  Score 26;  DB 2;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALFG 19
              | |  |:| ||
Db          5 GSEVNLDAEFG 15


RESULT 10
US-09-394-019C-150
; Sequence 150, Application US/09394019C
; Patent No. 6936687
; GENERAL INFORMATION:
;  APPLICANT: Oncoimmunin, Inc.
;  APPLICANT:  Komoriya, Akira
;  APPLICANT:  Packard, Beverly
;  TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
;  TITLE OF INVENTION:  SAMPLES AND METHODS OF USE THEREOF
;  FILE REFERENCE: 300-903820US
;  CURRENT APPLICATION NUMBER: US/09/394,019C
;  CURRENT FILING DATE:  1999-09-10
;  PRIOR APPLICATION NUMBER: PCT/US98/00300
;  PRIOR FILING DATE: 1998-02-20
;  PRIOR APPLICATION NUMBER: US 08/802,981
;  PRIOR FILING DATE: 1997-02-20
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 150
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide substrate
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: K is blocked with Fmoc
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: X is epsilon aminocaproic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: X is episilon-aminocaproic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-150

  Query Match             25.5%;  Score 26;  DB 2;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALFG 19
              | |  |:| ||
Db          5 GSEVNLDAEFG 15


RESULT 11
US-09-394-019C-395
; Sequence 395, Application US/09394019C
; Patent No. 6936687
; GENERAL INFORMATION:
;  APPLICANT: Oncoimmunin, Inc.
;  APPLICANT:  Komoriya, Akira
;  APPLICANT:  Packard, Beverly
;  TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
;  TITLE OF INVENTION:  SAMPLES AND METHODS OF USE THEREOF
;  FILE REFERENCE: 300-903820US
;  CURRENT APPLICATION NUMBER: US/09/394,019C
;  CURRENT FILING DATE:  1999-09-10
;  PRIOR APPLICATION NUMBER: PCT/US98/00300
;  PRIOR FILING DATE: 1998-02-20
;  PRIOR APPLICATION NUMBER: US 08/802,981
;  PRIOR FILING DATE: 1997-02-20
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 395
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial
```

```
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide.  Chemically synthesized protease substrate.
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: Xaa is episilon-aminocaproic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: Xaa is episilon-aminocaproic acid
US-09-394-019C-395

  Query Match             25.5%;  Score 26;  DB 2;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALFG 19
              | |   |:| ||
Db          5 GSEVNLDAEFG 15


RESULT 12
US-09-043-560B-8
; Sequence 8, Application US/09043560B
; Patent No. 6569833
; GENERAL INFORMATION:
;  APPLICANT:  Fahraeus, Robin
;  APPLICANT:  Lane, David P.
;  TITLE OF INVENTION:  Cyclin Dependent Kinase Binding Compounds
;  FILE REFERENCE:  CCI-003US
;  CURRENT APPLICATION NUMBER: US/09/043,560B
;  CURRENT FILING DATE:  1999-04-07
;  NUMBER OF SEQ ID NOS:  16
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-043-560B-8

  Query Match             24.5%;  Score 25;  DB 2;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+03;
  Matches    6;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 KGFEPTLEALFG 19
              :||  ||  | |
Db          5 EGFLDTLVVLHG 16


RESULT 13
US-09-171-432A-52
; Sequence 52, Application US/09171432A
; Patent No. 6838237
;  GENERAL INFORMATION:
;    APPLICANT:  Fields, Howard A.
;    APPLICANT:  Khudyakov, Yury E.
;    TITLE OF INVENTION:  Antigenically Reactive Regions of the
;    TITLE OF INVENTION:  Hepatitis A Virus Polyprotein
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kilpatrick Stockton LLP
;      STREET:  3424 Peachtree Road, N.E.
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30326
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/171,432A
;      FILING DATE:  23-NOV-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greene, Jamie L.
;      REGISTRATION NUMBER:  32,467
;      REFERENCE/DOCKET NUMBER:  03063-0231US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 949-2400
;      TELEFAX:  (404) 949-2499
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..20
;      OTHER INFORMATION:  /label= YK-1348
US-09-171-432A-52

  Query Match             24.5%;  Score 25;  DB 2;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+03;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         11 EPTLEALFGK 20
              || :   |:||
Db          3 EPVVCYLYGK 12


RESULT 14
US-09-743-209A-6
; Sequence 6, Application US/09743209A
; Patent No. 6905849
; GENERAL INFORMATION:
;  APPLICANT: Barton, Barry
;  APPLICANT:  McNaughton, Heather Jane
;  APPLICANT:  Schofield, Christopher Joseph
;  APPLICANT:  Thirkettle, Jan Edward
;  TITLE OF INVENTION: Process for Preparing Clavam Derivatives
;  TITLE OF INVENTION:  by Using Polypeptides Having Beta-Lactam Synthetase Activity
;  FILE REFERENCE: P32085
;  CURRENT APPLICATION NUMBER: US/09/743,209A
;  CURRENT FILING DATE:  2001-02-06
;  PRIOR APPLICATION NUMBER: GB 9815666.4
;  PRIOR FILING DATE: 1998-07-17
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: orf3 protein
US-09-743-209A-6

  Query Match             24.5%;  Score 25;  DB 2;  Length 20;
  Best Local Similarity   62.5%;  Pred. No. 1.8e+03;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         12 PTLEALFG 19
              | | | ||
Db          3 PVLPAAFG 10


RESULT 15
```

```
US-09-394-019C-123
; Sequence 123, Application US/09394019C
; Patent No. 6936687
; GENERAL INFORMATION:
;  APPLICANT: Oncoimmunin, Inc.
;  APPLICANT:  Komoriya, Akira
;  APPLICANT:  Packard, Beverly
;  TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
;  TITLE OF INVENTION:  SAMPLES AND METHODS OF USE THEREOF
;  FILE REFERENCE: 300-903820US
;  CURRENT APPLICATION NUMBER: US/09/394,019C
;  CURRENT FILING DATE:  1999-09-10
;  PRIOR APPLICATION NUMBER: PCT/US98/00300
;  PRIOR FILING DATE: 1998-02-20
;  PRIOR APPLICATION NUMBER: US 08/802,981
;  PRIOR FILING DATE: 1997-02-20
;  NUMBER OF SEQ ID NOS: 405
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide substrate
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: K is blocked with Fmoc
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: X is epsilon aminocaproic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (7)..(7)
;   OTHER INFORMATION: E is D form
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (10)..(10)
;   OTHER INFORMATION: L is D form
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (14)..(14)
;   OTHER INFORMATION: F is D form
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: X is episilon-aminocaproic acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16)..(16)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-123

  Query Match             24.5%;  Score 25;  DB 2;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 1.8e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALFG 19
              | |   |:| ||
Db          5 GSEVKLDAEFG 15


Search completed: March 21, 2006, 19:20:07
Job time : 47 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:29:44 ; Search time 161 Seconds
(without alignments)
51.904 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 16375

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	20	4	US-10-115-072-32	Sequence 32, Appl
2	102	100.0	20	4	US-10-679-032-70	Sequence 70, Appl
3	36	35.3	20	5	US-10-873-015-42	Sequence 42, Appl
4	32	31.4	20	3	US-09-864-761-46713	Sequence 46713, A
5	31	30.4	20	5	US-10-873-015-43	Sequence 43, Appl
6	30	29.4	20	4	US-10-226-007-438	Sequence 438, App
7	29	28.4	20	4	US-10-283-017-2077	Sequence 2077, Ap
8	28	27.5	20	4	US-10-226-007-437	Sequence 437, App
9	28	27.5	20	5	US-10-875-133-121	Sequence 121, App
10	28	27.5	20	5	US-10-875-133-122	Sequence 122, App
11	28	27.5	20	5	US-10-875-133-123	Sequence 123, App
12	28	27.5	20	5	US-10-875-133-124	Sequence 124, App
13	28	27.5	20	5	US-10-875-133-125	Sequence 125, App
14	28	27.5	20	5	US-10-875-133-126	Sequence 126, App
15	28	27.5	20	5	US-10-875-133-127	Sequence 127, App
16	28	27.5	20	5	US-10-875-133-128	Sequence 128, App
17	27	26.5	20	3	US-09-895-828-472	Sequence 472, App
18	27	26.5	20	3	US-09-962-756-1138	Sequence 1138, Ap
19	27	26.5	20	4	US-10-114-666-472	Sequence 472, App
20	27	26.5	20	4	US-10-414-692-53	Sequence 53, Appl
21	27	26.5	20	4	US-10-253-471-1138	Sequence 1138, Ap
22	27	26.5	20	4	US-10-253-493-1138	Sequence 1138, Ap
23	26.5	26.0	20	4	US-10-362-527-229	Sequence 229, App
24	26.5	26.0	20	6	US-11-005-794-193	Sequence 193, App
25	26	25.5	20	3	US-09-931-375A-81	Sequence 81, Appl
26	26	25.5	20	3	US-09-962-756-1132	Sequence 1132, Ap
27	26	25.5	20	3	US-09-747-287-198	Sequence 198, App
28	26	25.5	20	3	US-09-874-350A-164	Sequence 164, App
29	26	25.5	20	4	US-10-029-386-29951	Sequence 29951, A
30	26	25.5	20	4	US-10-253-471-1132	Sequence 1132, Ap
31	26	25.5	20	4	US-10-403-182-179	Sequence 179, App
32	26	25.5	20	4	US-10-253-493-1132	Sequence 1132, Ap
33	26	25.5	20	4	US-10-679-246-24	Sequence 24, Appl
34	26	25.5	20	5	US-10-690-276-656	Sequence 656, App
35	26	25.5	20	6	US-11-075-234-365	Sequence 365, App
36	25	24.5	20	3	US-09-171-432A-52	Sequence 52, Appl
37	25	24.5	20	3	US-09-833-245-145	Sequence 145, App
38	25	24.5	20	3	US-09-874-350A-137	Sequence 137, App
39	25	24.5	20	3	US-09-874-350A-138	Sequence 138, App
40	25	24.5	20	4	US-10-169-103-25	Sequence 25, Appl
41	25	24.5	20	4	US-10-286-964-8	Sequence 8, Appli
42	25	24.5	20	5	US-10-690-276-244	Sequence 244, App
43	25	24.5	20	5	US-10-690-276-546	Sequence 546, App
44	25	24.5	20	5	US-10-969-719A-152	Sequence 152, App
45	25	24.5	20	5	US-10-969-719A-176	Sequence 176, App

ALIGNMENTS

RESULT 1
US-10-115-072-32
; Sequence 32, Application US/10115072
; Publication No. US20030105003A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF
; TITLE OF INVENTION: ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY
; TITLE OF INVENTION: FOR DETERMINATION OF IMMUNE RESPONSES AGAINST OXIDIZED
; TITLE OF INVENTION: LOW DENSITY LIPOPROTEIN
; FILE REFERENCE: 03940.0057
; CURRENT APPLICATION NUMBER: US/10/115,072
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/281,410
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0101232-7
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0103754-8
; PRIOR FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-115-072-32

Query Match 100.0%; Score 102; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEIGLEGKGFEPTLEALFGK 20
||||||||||||||||||||
Db 1 IEIGLEGKGFEPTLEALFGK 20

RESULT 2
US-10-679-032-70
; Sequence 70, Application US/10679032
; Publication No. US20040202653A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: CARLSSON, ROLAND
; APPLICANT: BENGTSSON, JENNY
; APPLICANT: STRANDBERG, LEIF
; TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR

```
;  TITLE OF INVENTION:  TREATMENT OF ATHEROSCLEROSIS
;  FILE REFERENCE: 7303CIP
;  CURRENT APPLICATION NUMBER: US/10/679,032
;  CURRENT FILING DATE:  2003-10-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-679-032-70

  Query Match             100.0%;  Score 102;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 3
US-10-873-015-42
; Sequence 42, Application US/10873015
; Publication No. US20050032222A1
; GENERAL INFORMATION:
;  APPLICANT: Cham, Bill E.
;  APPLICANT:  Maltais, Jo-Ann B.
;  APPLICANT:  Bellotti, Marc
;  TITLE OF INVENTION: Modified Viral Particles with Immunogenic Properties and Reduced
;  TITLE OF INVENTION:  Lipid Content Useful for Treating and Preventing Infectious
;  TITLE OF INVENTION:  Diseases
;  FILE REFERENCE: 13131-0370 (44378-300773)
;  CURRENT APPLICATION NUMBER: US/10/873,015
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: US 10/601656
;  PRIOR FILING DATE: 2003-06-20
;  PRIOR APPLICATION NUMBER: US 10/311,679
;  PRIOR FILING DATE: 2002-12-18
;  PRIOR APPLICATION NUMBER: PCT/IB01/01099
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: PCT/AU00/01603
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: AU PQ8469
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 60/390,066
;  PRIOR FILING DATE: 2002-06-20
;  PRIOR APPLICATION NUMBER: US 60/491,928
;  PRIOR FILING DATE: 2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/542,947
;  PRIOR FILING DATE: 2004-02-09
;  PRIOR APPLICATION NUMBER: US 60/533,542
;  PRIOR FILING DATE: 2003-12-31
;  NUMBER OF SEQ ID NOS: 136
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Simian Immunodeficiency Virus
US-10-873-015-42

  Query Match             35.3%;  Score 36;  DB 5;  Length 20;
  Best Local Similarity   53.8%;  Pred. No. 1.1e+02;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 LEGKGFEPTLEAL 17
              |:| |  |||| :
Db          7 LKGLGVNPTLEEM 19


RESULT 4
US-09-864-761-46713
; Sequence 46713, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46713
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012072.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
US-09-864-761-46713

  Query Match             31.4%;  Score 32;  DB 3;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 4.9e+02;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 5
```

US-10-873-015-43
; Sequence 43, Application US/10873015
; Publication No. US20050032222A1
; GENERAL INFORMATION:
; APPLICANT: Cham, Bill E.
; APPLICANT: Maltais, Jo-Ann B.
; APPLICANT: Bellotti, Marc
; TITLE OF INVENTION: Modified Viral Particles with Immunogenic Properties and Reduced
; TITLE OF INVENTION: Lipid Content Useful for Treating and Preventing Infectious
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: 13131-0370 (44378-300773)
; CURRENT APPLICATION NUMBER: US/10/873,015
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 10/601656
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 10/311,679
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/IB01/01099
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: PCT/AU00/01603
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: AU PQ8469
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/390,066
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: US 60/491,928
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/542,947
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: US 60/533,542
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-10-873-015-43

Query Match 30.4%; Score 31; DB 5; Length 20;
Best Local Similarity 54.5%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 GKGFEPTLEAL 17
| | |||| :
Db 1 GLGVNPTLEEM 11

RESULT 6
US-10-226-007-438
; Sequence 438, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 438
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-10-226-007-438

Query Match 29.4%; Score 30; DB 4; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IGLEGKG 9
:||:|||
Db 1 LGLKGKG 7

RESULT 7
US-10-283-017-2077
; Sequence 2077, Application US/10283017
; Publication No. US20030211510A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C20
; CURRENT APPLICATION NUMBER: US/10/283,017
; CURRENT FILING DATE: 2002-10-28
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2077
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo spaiens
US-10-283-017-2077

Query Match 28.4%; Score 29; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 6 EGKGFEPTLEALFGK 20
|| | | :| |:
Db 3 EGAGCSPDAPSLSGR 17

RESULT 8
US-10-226-007-437
; Sequence 437, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 437
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Vesicular stomatitis virus
US-10-226-007-437

Query Match 27.5%; Score 28; DB 4; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          4 GLEGKG 9
              ||:|||
Db          1 GLKGKG 6


RESULT 9
US-10-875-133-121
; Sequence 121, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Coxacivirus -COXA9
US-10-875-133-121

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALF 18
              ||||||
Db          4 TLEALF 9


RESULT 10
US-10-875-133-122
; Sequence 122, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Coxacivirus -COXB1
US-10-875-133-122

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALF 18
              ||||||
Db          4 TLEALF 9


RESULT 11
US-10-875-133-123
; Sequence 123, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 123
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Coxacivirus -COXB5
US-10-875-133-123

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALF 18
              ||||||
Db          4 TLEALF 9


RESULT 12
US-10-875-133-124
; Sequence 124, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Echovirus  EC11G
US-10-875-133-124

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 TLEALF 18
              ||||||
Db          4 TLEALF 9


RESULT 13
US-10-875-133-125
; Sequence 125, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Coxacivirus -COXB4
US-10-875-133-125

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          13 TLEALF 18
               ||||||
Db           4 TLEALF 9


RESULT 14
US-10-875-133-126
; Sequence 126, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Swine Vesicular Disease Virus SVDVH
US-10-875-133-126

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 TLEALF 18
               ||||||
Db           4 TLEALF 9


RESULT 15
US-10-875-133-127
; Sequence 127, Application US/10875133
; Publication No. US20050048473A1
; GENERAL INFORMATION:
;  APPLICANT: Arad, Dorit
;  TITLE OF INVENTION: ENZYMATIC DIAGNOSTIC TEST FOR SARS AND OTHER VIRAL DISEASES
;  FILE REFERENCE: 12275/3
;  CURRENT APPLICATION NUMBER: US/10/875,133
;  CURRENT FILING DATE:  2004-06-23
;  PRIOR APPLICATION NUMBER: 60/480,605
;  PRIOR FILING DATE: 2003-06-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Swine Vesicular Disease Virus SVDVU
US-10-875-133-127

  Query Match             27.5%;  Score 28;  DB 5;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 TLEALF 18
               ||||||
Db           4 TLEALF 9


Search completed: March 21, 2006, 19:33:04
Job time : 162 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:30:29 ; Search time 23 Seconds
(without alignments)
24.889 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 1668

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	24.5	20	6	US-10-485-788A-590	Sequence 590, App
2	24.5	24.0	20	7	US-11-145-861-75	Sequence 75, Appl
3	24	23.5	20	6	US-10-623-155-249	Sequence 249, App
4	24	23.5	20	6	US-10-623-155-401	Sequence 401, App
5	24	23.5	20	6	US-10-623-155-509	Sequence 509, App
6	23	22.5	20	7	US-11-106-415-33	Sequence 33, Appl
7	22	21.6	20	6	US-10-623-155-533	Sequence 533, App
8	22	21.6	20	6	US-10-485-788A-619	Sequence 619, App
9	22	21.6	20	6	US-10-498-026-18	Sequence 18, Appl
10	22	21.6	20	7	US-11-022-562-290	Sequence 290, App
11	22	21.6	20	7	US-11-022-562-291	Sequence 291, App
12	22	21.6	20	7	US-11-022-562-292	Sequence 292, App
13	22	21.6	20	7	US-11-022-562-293	Sequence 293, App
14	21	20.6	20	6	US-10-623-155-402	Sequence 402, App
15	21	20.6	20	6	US-10-623-155-510	Sequence 510, App
16	21	20.6	20	6	US-10-623-155-532	Sequence 532, App
17	21	20.6	20	7	US-11-033-365-204	Sequence 204, App
18	21	20.6	20	7	US-11-054-515-2961	Sequence 2961, Ap
19	21	20.6	20	7	US-11-094-142-2	Sequence 2, Appli
20	21	20.6	20	7	US-11-094-142-8	Sequence 8, Appli
21	21	20.6	20	7	US-11-094-142-28	Sequence 28, Appl
22	21	20.6	20	7	US-11-033-039-840	Sequence 840, App
23	21	20.6	20	7	US-11-152-366-272	Sequence 272, App
24	21	20.6	20	7	US-11-200-822-11	Sequence 11, Appl
25	21	20.6	20	7	US-11-004-399-3259	Sequence 3259, Ap
26	20	19.6	20	6	US-10-986-501-219	Sequence 219, App
27	20	19.6	20	6	US-10-986-501-221	Sequence 221, App
28	20	19.6	20	6	US-10-623-155-545	Sequence 545, App
29	20	19.6	20	6	US-10-485-788A-559	Sequence 559, App
30	20	19.6	20	6	US-10-504-879-64	Sequence 64, Appl
31	20	19.6	20	6	US-10-504-879-65	Sequence 65, Appl
32	20	19.6	20	6	US-10-973-977-51	Sequence 51, Appl
33	20	19.6	20	6	US-10-973-977-57	Sequence 57, Appl
34	20	19.6	20	6	US-10-936-888-7	Sequence 7, Appli
35	20	19.6	20	6	US-10-936-888-8	Sequence 8, Appli
36	20	19.6	20	7	US-11-033-365-120	Sequence 120, App
37	20	19.6	20	7	US-11-033-365-202	Sequence 202, App
38	20	19.6	20	7	US-11-033-365-203	Sequence 203, App
39	20	19.6	20	7	US-11-033-365-205	Sequence 205, App
40	20	19.6	20	7	US-11-033-365-206	Sequence 206, App
41	20	19.6	20	7	US-11-033-365-208	Sequence 208, App
42	20	19.6	20	7	US-11-033-365-209	Sequence 209, App
43	20	19.6	20	7	US-11-033-365-210	Sequence 210, App
44	20	19.6	20	7	US-11-094-142-29	Sequence 29, Appl
45	20	19.6	20	7	US-11-032-951-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-485-788A-590
; Sequence 590, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 590
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-590

Query Match 24.5%; Score 25; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 EGKGF 10
              :||||
Db          8 QGKGF 12
```

RESULT 2
US-11-145-861-75
; Sequence 75, Application US/11145861
; Publication No. US20060014138A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul
; APPLICANT: Wang, Xiaoju
; TITLE OF INVENTION: Phage Microarray Profiling of the Humoral Response to Disease
; FILE REFERENCE: UM-09899
; CURRENT APPLICATION NUMBER: US/11/145,861
; CURRENT FILING DATE: 2005-06-06

```
;  NUMBER OF SEQ ID NOS: 464
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-145-861-75

  Query Match             24.0%;  Score 24.5;  DB 7;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 6.9e+02;
  Matches    6;  Conservative    4;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          3 IGLEGKGFEPTLEAL 17
              :|  |:| :| :| |
Db          4 LGNHGEG-KPIVECL 17


RESULT 3
US-10-623-155-249
; Sequence 249, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 249
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-249

  Query Match             23.5%;  Score 24;  DB 6;  Length 20;
  Best Local Similarity   62.5%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEA 16
              || | | |
Db          1 GFYPILNA 8


RESULT 4
US-10-623-155-401
; Sequence 401, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 401
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-401

  Query Match             23.5%;  Score 24;  DB 6;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 LEALFGK 20
              :||| ||
Db          5 IEALSGK 11


RESULT 5
US-10-623-155-509
; Sequence 509, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 509
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-509

  Query Match             23.5%;  Score 24;  DB 6;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         14 LEALFGK 20
              :||| ||
Db          5 IEALSGK 11


RESULT 6
US-11-106-415-33
; Sequence 33, Application US/11106415
; Publication No. US20050287153A1
; GENERAL INFORMATION:
;  APPLICANT: MARK S. DENNIS
;  TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
;  FILE REFERENCE: P1774R1P2
;  CURRENT APPLICATION NUMBER: US/11/106,415
;  CURRENT FILING DATE:  2005-04-13
;  PRIOR APPLICATION NUMBER: US 10/186,229
;  PRIOR FILING DATE: 2002-06-28
;  NUMBER OF SEQ ID NOS: 425
; SEQ ID NO 33
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: sequence is synthesized
US-11-106-415-33

  Query Match             22.5%;  Score 23;  DB 7;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLE 6
              :|:|||
Db         10 LEMGLE 15


RESULT 7
US-10-623-155-533
; Sequence 533, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
```

```
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 533
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-533

  Query Match             21.6%;  Score 22;  DB 6;  Length 20;
  Best Local Similarity   44.4%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFE 11
              || ||:  :
Db          3 IGKEGRNLK 11


RESULT 8
US-10-485-788A-619
; Sequence 619, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
;  APPLICANT: Lu, Peter S.
;  APPLICANT:  Rabinowitz, Joshua D.
;  APPLICANT:  Schweizer, Johannes
;  APPLICANT:  Carrick, Deanna Marie
;  APPLICANT:  Arbor Vita Corporation
;  TITLE OF INVENTION: Molecular Interactions in Cells
;  FILE REFERENCE: 20054-003320US
;  CURRENT APPLICATION NUMBER: US/10/485,788A
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: US 60/309,841
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/360,061
;  PRIOR FILING DATE: 2002-02-25
;  PRIOR APPLICATION NUMBER: WO PCT/US02/24655
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 841
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 619
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human T-lymphotropic virus 1
US-10-485-788A-619

  Query Match             21.6%;  Score 22;  DB 6;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+03;
  Matches    5;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEALF 18
              | ||  |  |
Db          6 GLEPPSEKHF 15


RESULT 9
US-10-498-026-18
; Sequence 18, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
;  APPLICANT: CIRCASSIA LIMITED
;  TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
;  FILE REFERENCE: N.87430 WO GCW
;  CURRENT APPLICATION NUMBER: US/10/498,026
;  CURRENT FILING DATE:  2004-06-04
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (4)..(4)
;   OTHER INFORMATION: Xaa = any amino acid
US-10-498-026-18

  Query Match             21.6%;  Score 22;  DB 6;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 GFEPTLEA 16
              | :|  ||
Db          3 GXQPAAEA 10


RESULT 10
US-11-022-562-290
; Sequence 290, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
;  APPLICANT: Ruprecht, Ruth M.
;  APPLICANT:  Shisong, Jiang
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
;  TITLE OF INVENTION:  A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
;  FILE REFERENCE: DFN-043CN
;  CURRENT APPLICATION NUMBER: US/11/022,562
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: PCT/US03/20322
;  PRIOR FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 60/392718
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 340
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 290
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus
US-11-022-562-290

  Query Match             21.6%;  Score 22;  DB 7;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 LEGKGFEP 12
              :| | | |
Db          9 VEEKAFSP 16


RESULT 11
US-11-022-562-291
; Sequence 291, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
;  APPLICANT: Ruprecht, Ruth M.
;  APPLICANT:  Shisong, Jiang
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
;  TITLE OF INVENTION:  A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
;  FILE REFERENCE: DFN-043CN
;  CURRENT APPLICATION NUMBER: US/11/022,562
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: PCT/US03/20322
;  PRIOR FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 60/392718
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 340
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 291
;   LENGTH: 20
```

```
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus
US-11-022-562-291

  Query Match             21.6%;  Score 22;  DB 7;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 LEGKGFEP 12
              :| | | |
Db          9 VEEKAFSP 16


RESULT 12
US-11-022-562-292
; Sequence 292, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
;  APPLICANT: Ruprecht, Ruth M.
;  APPLICANT:  Shisong, Jiang
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
;  TITLE OF INVENTION:  A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
;  FILE REFERENCE: DFN-043CN
;  CURRENT APPLICATION NUMBER: US/11/022,562
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: PCT/US03/20322
;  PRIOR FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 60/392718
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 340
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 292
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus
US-11-022-562-292

  Query Match             21.6%;  Score 22;  DB 7;  Length 20;
  Best Local Similarity   36.4%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 KGFEPTLEALF 18
              | | | :  :|
Db          2 KAFSPEVIPMF 12


RESULT 13
US-11-022-562-293
; Sequence 293, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
;  APPLICANT: Ruprecht, Ruth M.
;  APPLICANT:  Shisong, Jiang
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
;  TITLE OF INVENTION:  A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
;  FILE REFERENCE: DFN-043CN
;  CURRENT APPLICATION NUMBER: US/11/022,562
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: PCT/US03/20322
;  PRIOR FILING DATE: 2003-06-27
;  PRIOR APPLICATION NUMBER: 60/392718
;  PRIOR FILING DATE: 2002-06-27
;  NUMBER OF SEQ ID NOS: 340
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Human Immunodeficiency Virus
US-11-022-562-293

  Query Match             21.6%;  Score 22;  DB 7;  Length 20;
  Best Local Similarity   36.4%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          8 KGFEPTLEALF 18
              | | | :  :|
Db          2 KAFSPEVIPMF 12


RESULT 14
US-10-623-155-402
; Sequence 402, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 402
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-402

  Query Match             20.6%;  Score 21;  DB 6;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+03;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFE 11
              :| | ||  |
Db          1 KIELHGKPIE 10


RESULT 15
US-10-623-155-510
; Sequence 510, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 510
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-155-510

  Query Match             20.6%;  Score 21;  DB 6;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+03;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFE 11
              :| | ||  |
Db          1 KIELHGKPIE 10


Search completed: March 21, 2006, 19:33:32
Job time : 24 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 19:19:29 ; Search time 554 Seconds
(without alignments)
49.890 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 46454

Minimum DB seq length: 20
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US066_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US073_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US074_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US075_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US076_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US077_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US078_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US079_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
20: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
21: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
22: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
23: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
24: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
25: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
26: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
27: /cgn2_6/ptodata/1/paa/US097_COMB.pep:*
28: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
29: /cgn2_6/ptodata/1/paa/US099_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
33: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
34: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
35: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
36: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
37: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
38: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
39: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
40: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
41: /cgn2_6/ptodata/1/paa/US111_COMB.pep:*
42: /cgn2_6/ptodata/1/paa/US112_COMB.pep:*
43: /cgn2_6/ptodata/1/paa/US114_COMB.pep:*
44: /cgn2_6/ptodata/1/paa/US600_COMB.pep:*
45: /cgn2_6/ptodata/1/paa/US601_COMB.pep:*
46: /cgn2_6/ptodata/1/paa/US602_COMB.pep:*
47: /cgn2_6/ptodata/1/paa/US603_COMB.pep:*
48: /cgn2_6/ptodata/1/paa/US604_COMB.pep:*
49: /cgn2_6/ptodata/1/paa/US605_COMB.pep:*
50: /cgn2_6/ptodata/1/paa/US606_COMB.pep:*
51: /cgn2_6/ptodata/1/paa/US607_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	20	31	US-10-115-072-32	Sequence 32, Appl
2	102	100.0	20	36	US-10-679-032-70	Sequence 70, Appl
3	36	35.3	20	31	US-10-111-983-867	Sequence 867, App
4	36	35.3	20	38	US-10-873-015-42	Sequence 42, Appl
5	35	34.3	20	31	US-10-111-983-15117	Sequence 15117, A
6	32	31.4	20	28	US-09-864-761-46713	Sequence 46713, A
7	32	31.4	20	31	US-10-182-997-22959	Sequence 22959, A
8	32	31.4	20	32	US-10-203-136-30647	Sequence 30647, A
9	32	31.4	20	32	US-10-203-139-29798	Sequence 29798, A
10	32	31.4	20	46	US-60-236-359-20130	Sequence 20130, A
11	31	30.4	20	38	US-10-873-015-43	Sequence 43, Appl
12	30	29.4	20	32	US-10-226-007-438	Sequence 438, App
13	29	28.4	20	1	PCT-US02-34777-2077	Sequence 2077, Ap
14	29	28.4	20	26	US-09-643-458B-11	Sequence 11, Appl
15	29	28.4	20	26	US-09-643-458C-11	Sequence 11, Appl
16	29	28.4	20	31	US-10-111-983-12732	Sequence 12732, A
17	29	28.4	20	31	US-10-111-983-12757	Sequence 12757, A
18	29	28.4	20	32	US-10-283-017-2077	Sequence 2077, Ap
19	28	27.5	20	1	PCT-US97-04635-17	Sequence 17, Appl
20	28	27.5	20	25	US-09-543-696-17	Sequence 17, Appl
21	28	27.5	20	25	US-09-543-696B-17	Sequence 17, Appl
22	28	27.5	20	32	US-10-226-007-437	Sequence 437, App
23	28	27.5	20	34	US-10-405-027-3005	Sequence 3005, Ap
24	28	27.5	20	38	US-10-875-133-121	Sequence 121, App
25	28	27.5	20	38	US-10-875-133-122	Sequence 122, App
26	28	27.5	20	38	US-10-875-133-123	Sequence 123, App
27	28	27.5	20	38	US-10-875-133-124	Sequence 124, App
28	28	27.5	20	38	US-10-875-133-125	Sequence 125, App
29	28	27.5	20	38	US-10-875-133-126	Sequence 126, App
30	28	27.5	20	38	US-10-875-133-127	Sequence 127, App
31	28	27.5	20	38	US-10-875-133-128	Sequence 128, App
32	28	27.5	20	45	US-60-195-311-830	Sequence 830, App
33	27	26.5	20	1	PCT-US02-30312-1138	Sequence 1138, Ap
34	27	26.5	20	1	PCT-US02-30412-1138	Sequence 1138, Ap
35	27	26.5	20	12	US-08-256-747B-2	Sequence 2, Appli
36	27	26.5	20	25	US-09-538-038-2082	Sequence 2082, Ap
37	27	26.5	20	25	US-09-538-038A-2082	Sequence 2082, Ap
38	27	26.5	20	28	US-09-895-828-472	Sequence 472, App
39	27	26.5	20	31	US-10-111-983-27122	Sequence 27122, A
40	27	26.5	20	31	US-10-114-666-472	Sequence 472, App
41	27	26.5	20	32	US-10-253-471-1138	Sequence 1138, Ap
42	27	26.5	20	32	US-10-253-471A-1138	Sequence 1138, Ap
43	27	26.5	20	32	US-10-253-471B-1138	Sequence 1138, Ap
44	27	26.5	20	32	US-10-253-493-1138	Sequence 1138, Ap
45	27	26.5	20	34	US-10-414-692-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-10-115-072-32
; Sequence 32, Application US/10115072
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN

```
;  APPLICANT:  SHAH, PREDIMAN K.
;  TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF
;  TITLE OF INVENTION:  ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY
;  TITLE OF INVENTION:  FOR DETERMINATION OF IMMUNE RESPONSES AGAINST OXIDIZED
;  TITLE OF INVENTION:  LOW DENSITY LIPOPROTEIN
;  FILE REFERENCE: 03940.0057
;  CURRENT APPLICATION NUMBER: US/10/115,072
;  CURRENT FILING DATE:  2002-08-20
;  PRIOR APPLICATION NUMBER: 60/281,410
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: SE 0101232-7
;  PRIOR FILING DATE: 2001-05-04
;  PRIOR APPLICATION NUMBER: SE 0103754-8
;  PRIOR FILING DATE: 2001-09-11
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-115-072-32

  Query Match             100.0%;  Score 102;  DB 31;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 2
US-10-679-032-70
; Sequence 70, Application US/10679032
; GENERAL INFORMATION:
;  APPLICANT: NILSSON, JAN
;  APPLICANT:  CARLSSON, ROLAND
;  APPLICANT:  BENGTSSON, JENNY
;  APPLICANT:  STRANDBERG, LEIF
;  TITLE OF INVENTION: PEPTIDE-BASED PASSIVE IMMUNIZATION THERAPY FOR
;  TITLE OF INVENTION:  TREATMENT OF ATHEROSCLEROSIS
;  FILE REFERENCE: 7303CIP
;  CURRENT APPLICATION NUMBER: US/10/679,032
;  CURRENT FILING DATE:  2003-10-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 70
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-10-679-032-70

  Query Match             100.0%;  Score 102;  DB 36;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db          1 IEIGLEGKGFEPTLEALFGK 20


RESULT 3
US-10-111-983-867
; Sequence 867, Application US/10111983
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT:  GALEOTTI Cesira
;  APPLICANT:  GRANDI Guido
;  APPLICANT:  MASIGNANI Vega
;  APPLICANT:  MORA Mariarosa
;  APPLICANT:  PIZZA Mariagrazia
;  APPLICANT:  RAPPUOLI Rino
;  APPLICANT:  RATTI Giulio
;  APPLICANT:  SCARLATO Vincenzo
;  APPLICANT:  SCARSELLI Maria
;  TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
;  FILE REFERENCE: 2300-1654  (PP01654.003)
;  CURRENT APPLICATION NUMBER: US/10/111,983
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US-60/162616
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 37764
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 867
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Neisseria
US-10-111-983-867

  Query Match             35.3%;  Score 36;  DB 31;  Length 20;
  Best Local Similarity   46.7%;  Pred. No. 1.2e+03;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              :|: | |  :|| ||
Db          4 KGQDFTPLRDALVGK 18


RESULT 4
US-10-873-015-42
; Sequence 42, Application US/10873015
; GENERAL INFORMATION:
;  APPLICANT: Cham, Bill E.
;  APPLICANT:  Maltais, Jo-Ann B.
;  APPLICANT:  Bellotti, Marc
;  TITLE OF INVENTION: Modified Viral Particles with Immunogenic Properties and Reduced
;  TITLE OF INVENTION:  Lipid Content Useful for Treating and Preventing Infectious
;  TITLE OF INVENTION:  Diseases
;  FILE REFERENCE: 13131-0370 (44378-300773)
;  CURRENT APPLICATION NUMBER: US/10/873,015
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: US 10/601656
;  PRIOR FILING DATE: 2003-06-20
;  PRIOR APPLICATION NUMBER: US 10/311,679
;  PRIOR FILING DATE: 2002-12-18
;  PRIOR APPLICATION NUMBER: PCT/IB01/01099
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: PCT/AU00/01603
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: AU PQ8469
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 60/390,066
;  PRIOR FILING DATE: 2002-06-20
;  PRIOR APPLICATION NUMBER: US 60/491,928
;  PRIOR FILING DATE: 2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/542,947
;  PRIOR FILING DATE: 2004-02-09
;  PRIOR APPLICATION NUMBER: US 60/533,542
;  PRIOR FILING DATE: 2003-12-31
;  NUMBER OF SEQ ID NOS: 136
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Simian Immunodeficiency Virus
US-10-873-015-42

  Query Match             35.3%;  Score 36;  DB 38;  Length 20;
  Best Local Similarity   53.8%;  Pred. No. 1.2e+03;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          5 LEGKGFEPTLEAL 17
              |:| |  |||| :
Db          7 LKGLGVNPTLEEM 19


RESULT 5
US-10-111-983-15117
; Sequence 15117, Application US/10111983
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT:  GALEOTTI Cesira
;  APPLICANT:  GRANDI Guido
;  APPLICANT:  MASIGNANI Vega
;  APPLICANT:  MORA Mariarosa
;  APPLICANT:  PIZZA Mariagrazia
;  APPLICANT:  RAPPUOLI Rino
;  APPLICANT:  RATTI Giulio
;  APPLICANT:  SCARLATO Vincenzo
;  APPLICANT:  SCARSELLI Maria
;  TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
;  FILE REFERENCE: 2300-1654  (PP01654.003)
;  CURRENT APPLICATION NUMBER: US/10/111,983
;  CURRENT FILING DATE:  2003-06-27
;  PRIOR APPLICATION NUMBER: US-60/162616
;  PRIOR FILING DATE: 1999-10-29
;  NUMBER OF SEQ ID NOS: 37764
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 15117
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Neisseria
US-10-111-983-15117

  Query Match             34.3%;  Score 35;  DB 31;  Length 20;
  Best Local Similarity   46.7%;  Pred. No. 1.8e+03;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              :|: | |  :|| ||
Db          4 KGQDFTPLRDALAGK 18


RESULT 6
US-09-864-761-46713
; Sequence 46713, Application US/09864761
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46713
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012072.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
US-09-864-761-46713

  Query Match             31.4%;  Score 32;  DB 28;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5e+03;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 7
US-10-182-997-22959
; Sequence 22959, Application US/10182997
; GENERAL INFORMATION:
;  APPLICANT: Molecular Dynamics, Inc.
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  ANALYSIS OF GENE EXPRESSION IN HELA
;  FILE REFERENCE: PB 0004 WO 10
;  CURRENT APPLICATION NUMBER: US/10/182,997
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 04 February 2000 (04.02.00)
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 26 May 2000 (26.05.00)
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 03 August 2000 (03.08.00)
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 03 October 2000 (03.10.00)
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 27 September 2000 (27.09.00)
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 21 September 2000 (21.09.00)
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 30 June 2000 (30.06.00)
;  NUMBER OF SEQ ID NOS: 26941
;  SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 22959
;   LENGTH: 20
```

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012072.1
;   FEATURE:
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
US-10-182-997-22959

  Query Match             31.4%;  Score 32;  DB 31;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5e+03;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 8
US-10-203-136-30647
; Sequence 30647, Application US/10203136
; GENERAL INFORMATION:
;  APPLICANT: Molecular Dynamics, Inc.
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  ANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER
;  FILE REFERENCE: PB 0004 WO 3
;  CURRENT APPLICATION NUMBER: US/10/203,136
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 04 February 2000 (04.02.00)
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 26 May 2000 (26.05.00)
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 03 August 2000 (03.08.00)
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 03 October 2000 (03.10.00)
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 27 September 2000 (27.09.00)
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 21 September 2000 (21.09.00)
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 30 June 2000 (30.06.00)
;  NUMBER OF SEQ ID NOS: 38578
;  SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 30647
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012072.1
;   FEATURE:
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
US-10-203-136-30647

  Query Match             31.4%;  Score 32;  DB 32;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5e+03;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 9
US-10-203-139-29798
; Sequence 29798, Application US/10203139
; GENERAL INFORMATION:
;  APPLICANT: Molecular Dynamics, Inc.
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER
;  FILE REFERENCE: PB 0004 WO 4
;  CURRENT APPLICATION NUMBER: US/10/203,139
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 04 February 2000 (04.02.00)
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 26 May 2000 (26.05.00)
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 03 August 2000 (03.08.00)
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 03 October 2000 (03.10.00)
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 27 September 2000 (27.09.00)
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 21 September 2000 (21.09.00)
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 30 June 2000 (30.06.00)
;  NUMBER OF SEQ ID NOS: 37156
;  SOFTWARE: Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 29798
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012072.1
;   FEATURE:
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
US-10-203-139-29798

  Query Match             31.4%;  Score 32;  DB 32;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5e+03;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 10
US-60-236-359-20130
; Sequence 20130, Application US/60236359
; GENERAL INFORMATION:
;  APPLICANT:  Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION:  HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE:  MDhMORF-4P
;  CURRENT APPLICATION NUMBER: US/60/236,359
;  CURRENT FILING DATE:  2000-09-27
;  PRIOR APPLICATION NUMBER:  US 60/207,456
;  PRIOR FILING DATE:  2000-05-26
;  NUMBER OF SEQ ID NOS:  21709
;  SOFTWARE:  Molecular Dynamics Sequence Listing Engine
; SEQ ID NO 20130
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC012072.1
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
US-60-236-359-20130

  Query Match             31.4%;  Score 32;  DB 46;  Length 20;
  Best Local Similarity   50.0%;  Pred. No. 5e+03;
  Matches    6;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy          1 IEIGLEGKGFEP 12
              : | || || :|
Db          2 LHIKLEAKGLKP 13


RESULT 11
US-10-873-015-43
; Sequence 43, Application US/10873015
; GENERAL INFORMATION:
;  APPLICANT: Cham, Bill E.
;  APPLICANT:  Maltais, Jo-Ann B.
;  APPLICANT:  Bellotti, Marc
;  TITLE OF INVENTION: Modified Viral Particles with Immunogenic Properties and Reduced
;  TITLE OF INVENTION:  Lipid Content Useful for Treating and Preventing Infectious
;  TITLE OF INVENTION:  Diseases
;  FILE REFERENCE: 13131-0370 (44378-300773)
;  CURRENT APPLICATION NUMBER: US/10/873,015
;  CURRENT FILING DATE:  2004-06-21
;  PRIOR APPLICATION NUMBER: US 10/601656
;  PRIOR FILING DATE: 2003-06-20
;  PRIOR APPLICATION NUMBER: US 10/311,679
;  PRIOR FILING DATE: 2002-12-18
;  PRIOR APPLICATION NUMBER: PCT/IB01/01099
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: PCT/AU00/01603
;  PRIOR FILING DATE: 2000-12-28
;  PRIOR APPLICATION NUMBER: AU PQ8469
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 60/390,066
;  PRIOR FILING DATE: 2002-06-20
;  PRIOR APPLICATION NUMBER: US 60/491,928
;  PRIOR FILING DATE: 2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/542,947
;  PRIOR FILING DATE: 2004-02-09
;  PRIOR APPLICATION NUMBER: US 60/533,542
;  PRIOR FILING DATE: 2003-12-31
;  NUMBER OF SEQ ID NOS: 136
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Simian Immunodeficiency Virus
US-10-873-015-43

  Query Match             30.4%;  Score 31;  DB 38;  Length 20;
  Best Local Similarity   54.5%;  Pred. No. 7.1e+03;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 GKGFEPTLEAL 17
              | |  |||| :
Db          1 GLGVNPTLEEM 11


RESULT 12
US-10-226-007-438
; Sequence 438, Application US/10226007
; GENERAL INFORMATION:
;  APPLICANT: Myriad Genetics, Inc.
;  APPLICANT:  Morham, Scott
;  APPLICANT:  Zavitz, Kenton
;  APPLICANT:  Hobden, Adrian
;  TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
;  FILE REFERENCE: 5005.01
;  CURRENT APPLICATION NUMBER: US/10/226,007
;  CURRENT FILING DATE:  2002-11-15
;  PRIOR APPLICATION NUMBER: US 60/313,883
;  PRIOR FILING DATE: 2001-08-21
;  NUMBER OF SEQ ID NOS: 1673
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 438
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Vesicular stomatitis virus
US-10-226-007-438

  Query Match             29.4%;  Score 30;  DB 32;  Length 20;
  Best Local Similarity   71.4%;  Pred. No. 1e+04;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 IGLEGKG 9
              :||:|||
Db          1 LGLKGKG 7


RESULT 13
PCT-US02-34777-2077
; Sequence 2077, Application PC/TUS0234777
; GENERAL INFORMATION:
;  APPLICANT: Corixa Corporation
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.47803PC
;  CURRENT APPLICATION NUMBER: PCT/US02/34777
;  CURRENT FILING DATE:  2002-10-28
;  NUMBER OF SEQ ID NOS: 2157
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2077
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo spaiens
PCT-US02-34777-2077

  Query Match             28.4%;  Score 29;  DB 1;  Length 20;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+04;
  Matches    6;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              || |  |   :| |:
Db          3 EGAGCSPDAPSLSGR 17


RESULT 14
US-09-643-458B-11
; Sequence 11, Application US/09643458B
; GENERAL INFORMATION:
;  APPLICANT: Mytych, Daniel T
;  APPLICANT:  Swanson, Steven J
;  TITLE OF INVENTION: METHODS AND REAGENTS FOR THE DETECTION OF ANTIBODIES TO ADENOVIRI
;  FILE REFERENCE: JB0976-Q-US
;  CURRENT APPLICATION NUMBER: US/09/643,458B
;  CURRENT FILING DATE:  2000-08-22
;  PRIOR APPLICATION NUMBER: 60/150,622
;  PRIOR FILING DATE: 1999-08-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: peptide for detection of adenovirus antibody
US-09-643-458B-11
```

```
  Query Match             28.4%;  Score 29;  DB 26;  Length 20;
  Best Local Similarity   33.3%;  Pred. No. 1.4e+04;
  Matches    5;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              :|||:|  :    |:
Db          2 KGKGYETEINHAAGR 16


RESULT 15
US-09-643-458C-11
; Sequence 11, Application US/09643458C
; GENERAL INFORMATION:
;  APPLICANT: Mytych, Daniel T
;  APPLICANT:  Swanson, Steven J
;  TITLE OF INVENTION: METHODS AND REAGENTS FOR THE DETECTION OF ANTIBODIES TO ADENOVIRU
;  FILE REFERENCE: JB0976-Q-US
;  CURRENT APPLICATION NUMBER: US/09/643,458C
;  CURRENT FILING DATE:  2000-08-22
;  PRIOR APPLICATION NUMBER: 60/150,622
;  PRIOR FILING DATE: 1999-08-25
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: peptide for detection of adenovirus antibody
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: 20
;   OTHER INFORMATION: AMIDATION
US-09-643-458C-11

  Query Match             28.4%;  Score 29;  DB 26;  Length 20;
  Best Local Similarity   33.3%;  Pred. No. 1.4e+04;
  Matches    5;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          6 EGKGFEPTLEALFGK 20
              :|||:|  :    |:
Db          2 KGKGYETEINHAAGR 16


Search completed: March 21, 2006, 19:29:27
Job time : 555 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 18:52:28 ; Search time 38 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	4563	1	LPHUB	apolipoprotein B-1
2	98	96.1	385	2	A27001	apolipoprotein B -
3	50	49.0	159	2	G97066	phosphotransferase
4	48	47.1	465	1	WMBE44	maturation protein
5	48	47.1	465	1	WMBEZ8	UL38 protein - hum
6	46	45.1	231	2	C43727	conserved hypothet
7	46	45.1	326	2	E86632	pyruvate dehydroge
8	46	45.1	746	2	C95110	competence protein
9	46	45.1	746	2	A97979	competence protein
10	46	45.1	920	2	JC7313	aryl hydrocarbon r
11	45	44.1	106	2	D69447	hypothetical prote
12	45	44.1	243	2	AI3422	superoxide dismuta
13	45	44.1	323	2	E71134	hypothetical prote
14	45	44.1	344	2	S76268	probable UDP-3-O-[
15	45	44.1	397	2	AC3521	replication protei
16	45	44.1	440	2	C84265	adenylosuccinate s
17	44.5	43.6	190	1	C70435	gliding motility p
18	44	43.1	195	2	G83629	hypothetical prote
19	44	43.1	260	2	AI0800	lysine-arginine-or
20	44	43.1	311	2	S74459	iron(III) dicitrat
21	44	43.1	315	2	T12729	structural protein
22	44	43.1	503	2	AB2938	alpha-L-arabinofur
23	44	43.1	503	2	E98344	hypothetical prote
24	44	43.1	503	2	A95359	Probable ABC trans
25	44	43.1	1125	2	E90598	membrane nuclease,
26	43.5	42.6	309	2	I51900	carbonic anhydrase
27	43	42.2	227	2	H82005	hypothetical prote
28	43	42.2	260	1	JKEBT	lysine/arginine/or
29	43	42.2	262	2	AF0338	histidine-binding
30	43	42.2	535	1	I39730	NADH2 dehydrogenas
31	43	42.2	655	2	C95220	trehalose PTS syst
32	43	42.2	664	1	B32243	phosphotransferase
33	43	42.2	705	2	A99084	phosphotransferase
34	42.5	41.7	292	2	T06201	xyloglucan endo-1,
35	42.5	41.7	305	2	G84568	probable xylogluca
36	42.5	41.7	1358	2	T22695	hypothetical prote
37	42	41.2	94	2	T35283	hypothetical prote
38	42	41.2	263	2	T29458	probable two-compo
39	42	41.2	313	2	AC2873	hypothetical prote
40	42	41.2	379	2	T47262	butyryl-CoA dehydr
41	42	41.2	379	2	F97233	butyryl-CoA dehydr
42	42	41.2	397	2	H84225	acyl-CoA dehydroge
43	42	41.2	397	2	A75503	hypothetical prote
44	42	41.2	456	2	AF3637	butyryl-CoA dehydr
45	42	41.2	616	2	E97649	probable permease

ALIGNMENTS

RESULT 1
LPHUB
apolipoprotein B-100 precursor - human
N;Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 31-Dec-2004
C;Accession: A27850; A25679; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A26
4452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sco
DNA 6, 363-372, 1987
A;Title: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Accession: A27850
A;Molecule type: DNA
A;Residues: 1-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'
A;Cross-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMN0; UNIP
R;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A;Reference number: A91058; MUID:87161758; PMID:3030729
A;Accession: A25679
A;Molecule type: mRNA
A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA>
A;Cross-references: UNIPARC:UPI000017CF2E
A;Note: 1109-Asp was also found
R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McCa
Nucleic Acids Res. 14, 7501-7503, 1986
A;Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A;Reference number: A93639; MUID:87016385; PMID:3763409
A;Accession: A25263
A;Molecule type: mRNA
A;Residues: 1-272,'N',274-617,'A',619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A;Cross-references: UNIPARC:UPI000013C498; GB:X04506; NID:g34330; PIDN:CAA28191.1; PID:g
R;Law, S.W.; Grant, S.M.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A;Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A;Reference number: A94134; MUID:87041416; PMID:3464946
A;Accession: A25267
A;Molecule type: mRNA
A;Residues: 1-617,'A',619-703,'P',705-792,'R',794-1270,'S',1272-1866,'G',1868-2036,'N',2
4189-4220,'M',4222-4563 <LAW>
A;Cross-references: UNIPARC:UPI000017CF2F
A;Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
R;Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
J. Biol. Chem. 261, 12918-12921, 1986
A;Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A;Reference number: A92556; MUID:87008488; PMID:3759943
A;Accession: A25266
A;Molecule type: mRNA
A;Residues: 1-97,'I',99-328,'V',330-644,'I',646-918,'P',920-3318,'D',3320-3426,'T',3428-
9-4132,'G',4134-4180,'E',4182-4563 <CHE>
A;Cross-references: UNIPARC:UPI0000168754; GB:J02610; NID:g178803; PIDN:AAA35549.1; PID:

A;Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
R;Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
A;Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A;Reference number: A24320; MUID:86287319; PMID:3461454
A;Accession: A24320
A;Molecule type: mRNA
A;Residues: 1-97,'I',99-617,'A',619-941,'YYIWSLPPKP',951-1138,'PTGRLPNCFSNGLICYSLWLHSFQE
A;Cross-references: UNIPARC:UPI000016A571; GB:M14081; NID:g178795; PIDN:AAA51752.1; PID:
R;Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A;Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A;Reference number: A24684; MUID:86094221; PMID:3001697
A;Accession: A24684
A;Molecule type: mRNA
A;Residues: 485-617,'A',619-1044 <LA2>
A;Cross-references: UNIPARC:UPI0000071E20; GB:M12480; NID:g178791; PIDN:AAA51751.1; PID:
R;Protter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A;Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr
A;Reference number: A94088; MUID:86149325; PMID:3513177
A;Accession: A23817
A;Molecule type: mRNA
A;Residues: 1-291 <PRO>
A;Cross-references: UNIPARC:UPI000016A572; GB:M12681; NID:g178797; PIDN:AAA51753.1; PID:
R;Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
Proc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
A;Title: A partial cDNA clone for human apoliprotein B.
A;Reference number: A25774; MUID:85270450; PMID:3860836
A;Accession: A25774
A;Molecule type: mRNA
A;Residues: 709-791,'SSSWKAASHGCPHSAGD',810-906 <DEE>
A;Cross-references: UNIPARC:UPI000016A578; GB:K03175; NID:g178821; PIDN:AAA51759.1; PID:
R;Carlsson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G.
Gene 49, 29-51, 1986
A;Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74 reg
A;Reference number: A91565; MUID:87191999; PMID:2883086
A;Accession: A26533
A;Molecule type: mRNA
A;Residues: 1282-2721,2742-3290,'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A;Cross-references: UNIPARC:UPI00000728DB; GB:M15421; NID:g178817; PIDN:AAA51758.1; PID:
R;Hardman, D.A.; Protter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana
Biochemistry 26, 5478-5486, 1987
A;Title: Structural comparison of human apolipoproteins B-48 and B-100.
A;Reference number: A29671; MUID:88050832; PMID:3676265
A;Accession: A29671
A;Molecule type: mRNA
A;Residues: 1671-2323,'PYW',2327-2352,'H',2354-2398 <HAR>
A;Cross-references: UNIPARC:UPI00000729F0; GB:M17367; NID:g178731; PIDN:AAA51741.1; PID:
R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.;
Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on
A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Accession: A29287
A;Molecule type: mRNA
A;Residues: 3846-4298 <SHO>
A;Cross-references: UNIPARC:UPI0000173FDB
R;Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A;Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec
A;Reference number: A25572; MUID:87076044; PMID:3024665
A;Accession: A25572
A;Molecule type: mRNA
A;Residues: 4219-4337,'S',4339-4563 <PFI>
A;Cross-references: UNIPARC:UPI0000173FDC; GB:M36676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A;Reference number: A24738; MUID:86042646; PMID:2932736
A;Accession: A24738
A;Molecule type: mRNA
A;Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39
A;Cross-references: UNIPARC:UPI0000072661; GB:M12413; NID:g178735; PIDN:AAA51742.1; PID:
R;Chen, S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai
Science 238, 363-366, 1987
A;Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A;Reference number: A40133; MUID:88018019; PMID:3659919
A;Accession: B40133
A;Molecule type: mRNA
A;Residues: 2165-2179 <CH1>
A;Cross-references: UNIPARC:UPI000006FB19; GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:
A;Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
A;Accession: A40133
A;Molecule type: protein
A;Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55
36;1486-1498;1537-1556;1563-1572;1601-1610;1647-1661;1697-1724;1770-1781;1859-1897;1968-
A;Cross-references: UNIPARC:UPI0000173FEA; UNIPARC:UPI0000173FEB; UNIPARC:UPI0000173FEC;
FF1; UNIPARC:UPI0000173FF2; UNIPARC:UPI0000173FF3; UNIPARC:UPI0000173FF4; UNIPARC:UPI000
I0000173FFA; UNIPARC:UPI0000173FFB; UNIPARC:UPI0000173FFC; UNIPARC:UPI0000173FFD; UNIPAR
A;Note: these fragments were derived from apo48
R;Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
Biochem. Biophys. Res. Commun. 149, 1214-1219, 1987
A;Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism p
A;Reference number: A28002; MUID:88106542; PMID:3426612
A;Accession: A28002
A;Molecule type: mRNA
A;Residues: 2129-2179,2181-2235 <HA2>
A;Cross-references: UNIPARC:UPI0000173FFF; GB:M18471
A;Experimental source: intestine
A;Note: this mRNA from intestine includes a stop codon created by RNA editing in place o
R;Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, T
Nucleic Acids Res. 13, 6937-6953, 1985
A;Title: Human apolipoprotein B: identification of cDNA clones and characterization of m
A;Reference number: A24269; MUID:86041888; PMID:3903660
A;Accession: A24269
A;Molecule type: mRNA
A;Residues: 3056-3159 <MEH>
A;Cross-references: UNIPARC:UPI000016A575; GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g
R;Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A;Title: Identification of a novel in-frame translational stop codon in human intestine
A;Reference number: A29659; MUID:88049670; PMID:2445342
A;Accession: A29659
A;Molecule type: mRNA
A;Residues: 2169-2179 <HOS>
A;Cross-references: UNIPARC:UPI0000174000
A;Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A;Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest
ch encodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA,
R;Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
A;Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap
A;Reference number: A35783; MUID:90319144; PMID:2115173
A;Contents: disulfide bonds
A;Accession: A35783
A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5

A;Cross-references: UNIPARC:UPI0000174001; UNIPARC:UPI0000174002; UNIPARC:UPI0000174003;
008; UNIPARC:UPI0000174009; UNIPARC:UPI000017400A; UNIPARC:UPI000017400B; UNIPARC:UPI000
I0000174011; UNIPARC:UPI0000174012
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su
R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J.
FEBS Lett. 170, 105-108, 1984
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
A;Accession: A22006
A;Molecule type: protein
A;Residues: 873-892,'K',894-896 <LE1>
A;Cross-references: UNIPARC:UPI0000174013
A;Accession: B22006
A;Molecule type: protein
A;Residues: 3113,'L',3115-3130,'R',3132-3133,'P',3135-3136,'R' <LE2>
A;Cross-references: UNIPARC:UPI0000174013
R;Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.;
J. Biol. Chem. 261, 15364-15367, 1986
A;Title: Structure of the human apolipoprotein B gene.

```
A;Reference number: A92564; MUID:87057153; PMID:2946672
A;Contents: annotation; gene structure
R;Wagener, R.; Pfitzner, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
A;Title: Studies on the organization of the human apolipoprotein B 100 gene.
A;Reference number: A90715; MUID:87271140; PMID:2886136
A;Contents: annotation; gene structure
R;Weisgraber, K.H.; Rall Jr., S.C.
J. Biol. Chem. 262, 11097-11103, 1987
A;Title: Human apolipoprotein B-100 heparin-binding sites.
A;Reference number: A92605; MUID:87280197; PMID:3301850
A;Contents: annotation; heparin binding and disulfide bond
R;Dashti, N.; Lee, D.M.; Mok, T.
Biochem. Biophys. Res. Commun. 137, 493-499, 1986

  Query Match             100.0%;  Score 102;  DB 1;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 3e-07;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 2
A27001
apolipoprotein B - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 31-Dec-1993
C;Accession: A27001
R;Matsumoto, A.; Aburatani, H.; Shibasaki, Y.; Kodama, T.; Takaku, F.; Itakura, H.
Biochem. Biophys. Res. Commun. 142, 92-99, 1987
A;Title: Cloning and regulation of rat apolipoprotein B mRNA.
A;Reference number: A27001; MUID:87128110; PMID:3028408
A;Accession: A27001
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-385 <MAT>
A;Cross-references: UNIPARC:UPI000017778A
C;Superfamily: apolipoprotein B
C;Keywords: lipid binding; lipoprotein

  Query Match             96.1%;  Score 98;  DB 2;  Length 385;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFGK 20
              |||||||||||||||||||
Db         68 EIGLEGKGFEPTLEALFGK 86


RESULT 3
G97066
phosphotransferase system IIA component [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97066
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-159 <KUR>
A;Cross-references: UNIPROT:Q97JD2; UNIPARC:UPI00000CA18A; GB:AE001437; PIDN:AAK79322.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1354
C;Superfamily: phosphotransferase system glucose-specific enzyme II, factor III; phospho

  Query Match             49.0%;  Score 50;  DB 2;  Length 159;
  Best Local Similarity   69.2%;  Pred. No. 1.6;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFEPTLE 15
              : ||||||| :|
Db         85 VKLEGKGFEPLVE 97


RESULT 4
WMBE44
maturation protein - human herpesvirus 1 (strain A44)
C;Species: human herpesvirus 1
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31478
R;Pertuiset, B.; Boccara, M.; Cebrian, J.; Berthelot, N.; Chousterman, S.; Puvion-Dutill
J. Virol. 63, 2169-2179, 1989
A;Title: Physical mapping and nucleotide sequence of a herpes simplex virus type 1 gene
A;Reference number: A31478; MUID:89199774; PMID:2539510
A;Accession: A31478
A;Molecule type: DNA
A;Residues: 1-465 <PER>
A;Cross-references: UNIPROT:P17586; UNIPARC:UPI0000138B94; GB:M22962; GB:M18454; NID:g33
C;Superfamily: varicella-zoster virus gene 20 protein
C;Keywords: capsid assembly; DNA binding

  Query Match             47.1%;  Score 48;  DB 1;  Length 465;
  Best Local Similarity   50.0%;  Pred. No. 10;
  Matches   10;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              |:  |  :| || || |||:
Db        329 IKSQLPPRGLEPALERLFGR 348


RESULT 5
WMBEZ8
UL38 protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: B30088
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Per
J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: B30088
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-465 <MCG>
A;Cross-references: UNIPROT:P32888; UNIPARC:UPI0000138B93; GB:X14112; NID:g1944536; PIDN
C;Genetics:
A;Gene: UL38
C;Superfamily: varicella-zoster virus gene 20 protein
C;Keywords: capsid assembly; DNA binding

  Query Match             47.1%;  Score 48;  DB 1;  Length 465;
  Best Local Similarity   50.0%;  Pred. No. 10;
  Matches   10;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              |:  |  :| || || |||:
Db        329 IKSQLPPRGLEPALERLFGR 348


RESULT 6
C43727
conserved hypothetical protein ylxW - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 03-Mar-1993 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S26502; C43727; F69882
R;Beall, B.; Lutkenhaus, J.
J. Bacteriol. 171, 6821-6834, 1989
A;Title: Nucleotide sequence and insertional inactivation of a Bacillus subtilis gene th
```

```
A;Reference number: S26499; MUID:90078133; PMID:2556375
A;Accession: S26502
A;Molecule type: DNA
A;Residues: 1-231 <BEA>
A;Cross-references: UNIPROT:Q45543; UNIPARC:UPI0000060380; EMBL:M31827; NID:g142831; PID
R;Harry, E.J.; Wake, R.G.
J. Bacteriol. 171, 6835-6839, 1989
A;Title: Cloning and expression of a Bacillus subtilis division initiation gene for whic
A;Reference number: A43727; MUID:90078134; PMID:2556376
A;Accession: C43727
A;Molecule type: DNA
A;Residues: 1-107 <HAR>
A;Cross-references: UNIPARC:UPI00000B0918; GB:M31800; NID:g142848; PIDN:AAA22394.1; PID:
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69882
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-231 <KUN>
A;Cross-references: UNIPARC:UPI0000060380; GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CA
A;Experimental source: strain 168
C;Genetics:
A;Gene: ylxW
A;Start codon: TTG

  Query Match             45.1%;  Score 46;  DB 2;  Length 231;
  Best Local Similarity   57.1%;  Pred. No. 10;
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLE 15
              |:|::|:| | |||
Db        101 EVGVQGEGVEVTLE 114


RESULT 7
E86632
pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain [imported] - Lactococcus lact
N;Alternate names: PDH E1 component beta subunit
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 12-Jul-2004
C;Accession: E86632
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: E86632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <STO>
A;Cross-references: UNIPROT:Q9CJD6; UNIPARC:UPI00000C6736; GB:AE005176; PID:g12722902; P
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: pdhB
C;Superfamily: pyruvate dehydrogenase, E1 component, beta subunit
C;Keywords: oxidoreductase

  Query Match             45.1%;  Score 46;  DB 2;  Length 326;
  Best Local Similarity   52.9%;  Pred. No. 15;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFEPTLEALFG 19
              |||  :|| | :|  ||
Db         68 IGLATQGFHPIMEIQFG 84


RESULT 8
C95110
competence protein CelB [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95110
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-746 <KUR>
A;Cross-references: UNIPROT:Q97R74; UNIPARC:UPI00000C9CB0; GB:AE005672; PIDN:AAK75076.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0955
C;Superfamily: competence protein ComEC

  Query Match             45.1%;  Score 46;  DB 2;  Length 746;
  Best Local Similarity   61.1%;  Pred. No. 37;
  Matches   11;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFG 19
              |||||||  ||  :  ||
Db        136 EIGLEGKLSEPEGQRNFG 153


RESULT 9
A97979
competence protein [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: A97979
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A97979
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-746 <KUR>
A;Cross-references: UNIPROT:Q8DQ40; UNIPARC:UPI00000E353A; GB:AE007317; PIDN:AAK99661.1;
C;Genetics:
A;Gene: celB
C;Superfamily: competence protein ComEC

  Query Match             45.1%;  Score 46;  DB 2;  Length 746;
  Best Local Similarity   61.1%;  Pred. No. 37;
  Matches   11;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFG 19
              |||||||  ||  :  ||
Db        136 EIGLEGKLSEPEGQRNFG 153


RESULT 10
JC7313
aryl hydrocarbon receptor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
```

```
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
C;Accession: JC7313
R;Korkalainen, M.; Tuomisto, J.; Pohjanvirta, R.
Biochem. Biophys. Res. Commun. 273, 272-281, 2000
A;Title: Restructured transactivation domain in hamster AH receptor.
A;Reference number: JC7313
A;Accession: JC7313
A;Molecule type: mRNA
A;Residues: 1-920 <KOR>
A;Cross-references: UNIPROT:Q9JHY9; UNIPARC:UPI00000E7BB9
C;Comment: This receptor, a ligand-activated transcription factor, belongs to a family o
of 2,3,7,8-tetrachlorodibenzo-dioxin.
C;Genetics:
A;Gene: ahr
C;Keywords: DNA binding; receptor; transcription regulation

  Query Match             45.1%;  Score 46;  DB 2;  Length 920;
  Best Local Similarity   61.5%;  Pred. No. 46;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTL 14
              :: | ||||||:|
Db        790 QLDLPGKGFEPSL 802


RESULT 11
D69447
hypothetical protein AF1581 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69447
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69447
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-106 <KLE>
A;Cross-references: UNIPROT:O28691; UNIPARC:UPI0000056C84; GB:AE000993; GB:AE000782; NID
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF1581

  Query Match             44.1%;  Score 45;  DB 2;  Length 106;
  Best Local Similarity   50.0%;  Pred. No. 6.3;
  Matches   10;  Conservative    4;  Mismatches    2;  Indels    4;  Gaps    1;

Qy          5 LEGKGFEPTLEA----LFGK 20
              :|||||  |::|    |:||
Db          1 MEGKGFRHTVKAKTVVLYGK 20


RESULT 12
AI3422
superoxide dismutase (EC 1.15.1.1) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AI3422
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3422
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-243 <KUR>
A;Cross-references: UNIPROT:Q8YFZ5; UNIPARC:UPI0000058040; GB:AE008917; PIDN:AAL52548.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1367
A;Map position: I
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: oxidoreductase

  Query Match             44.1%;  Score 45;  DB 2;  Length 243;
  Best Local Similarity   52.9%;  Pred. No. 16;
  Matches    9;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          4 GLEGKGFEPTLEALFGK 20
              ||||| |  ::  |||
Db         91 GLEGKSLEEIVKESFGK 107


RESULT 13
E71134
hypothetical protein PH0841 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: E71134
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71134
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-323 <KAW>
A;Cross-references: UNIPROT:O58571; UNIPARC:UPI0000062F08; GB:AP000003; NID:g3236130; P
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0841

  Query Match             44.1%;  Score 45;  DB 2;  Length 323;
  Best Local Similarity   56.2%;  Pred. No. 21;
  Matches    9;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEAL 17
              |:||||:   | || |
Db        126 EVGLEGRKIYPYLETL 141


RESULT 14
S76268
probable UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.-) - Syne
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76268
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-344 <KAN>
A;Cross-references: UNIPROT:Q55612; UNIPARC:UPI000012E906; EMBL:D64000; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
C;Keywords: acyltransferase

  Query Match             44.1%;  Score 45;  DB 2;  Length 344;
  Best Local Similarity   62.5%;  Pred. No. 23;
  Matches   10;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFEPTLEALF 18
              || || || || |  |
Db        187 IGAEGFGFVPTPEGWF 202
```

RESULT 15
AC3521
replication protein a [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AC3521
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AC3521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Cross-references: UNIPROT:Q8YDT2; UNIPARC:UPI000005834C; GB:AE008918; PIDN:AAL53334.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0093
A;Map position: II
C;Superfamily: sopA protein

  Query Match 44.1%; Score 45; DB 2; Length 397;
  Best Local Similarity 61.5%; Pred. No. 27;
  Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 EIGLEGKGFEPTL 14
              :: ||||| |||:
Db         64 KLHLEGKGVEPTI 76
```

Search completed: March 21, 2006, 18:56:54
Job time : 40 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 18:49:07 ; Search time 235 Seconds
(without alignments)
60.045 Million cell updates/sec

Title: US-10-679-032-70
Perfect score: 102
Sequence: 1 IEIGLEGKGFEPTLEALFGK 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	102	100.0	825	2	Q7Z7Q0_HUMAN	Q7z7q0 homo sapien
2	102	100.0	3929	2	Q4ZG63_HUMAN	Q4zg63 homo sapien
3	102	100.0	4563	1	APOB_HUMAN	P04114 homo sapien
4	98	96.1	1477	2	Q8CGG8_MOUSE	Q8cgg8 mus musculu
5	98	96.1	4743	2	Q7TMA5_RAT	Q7tma5 rattus norv
6	93	91.2	103	2	Q9I8I1_DICLA	Q9i8i1 dicentrarch
7	90	88.2	2674	2	Q4S6S1_TETNG	Q4s6s1 tetraodon n
8	74	72.5	1763	2	Q9TUI6_MONDO	Q9tui6 monodelphis
9	70	68.6	3730	2	Q5TZ29_BRARE	Q5tz29 brachydanio
10	51	50.0	199	2	Q57EG8_BRUAB	Q57eg8 brucella ab
11	51	50.0	2534	2	Q762M9_9EUCA	Q762m9 pandalus hy
12	50	49.0	159	2	Q97JD2_CLOAB	Q97jd2 clostridium
13	49	48.0	314	1	Y3508_XANAC	Q8pgv3 xanthomonas
14	48	47.1	284	2	Q9LLC2_ASPOF	Q9llc2 asparagus o
15	48	47.1	449	2	Q6AB55_PROAC	Q6ab55 propionibac
16	48	47.1	465	1	VP19_HHV11	P32888 human herpe
17	48	47.1	465	1	VP19_HHV14	P17586 human herpe
18	48	47.1	1269	2	Q6CEW6_YARLI	Q6cew6 yarrowia li
19	48	47.1	1393	2	Q5BEJ1_EMENI	Q5bej1 aspergillus
20	48	47.1	1407	2	Q6MYM9_ASPFU	Q6mym9 aspergillus
21	48	47.1	1407	2	Q4WSJ5_ASPFU	Q4wsj5 aspergillus
22	47.5	46.6	445	1	GSDM1_HUMAN	Q96qa5 homo sapien
23	47.5	46.6	445	2	Q86VE7_HUMAN	Q86ve7 homo sapien
24	47	46.1	185	2	Q847K9_9CHLA	Q847k9 simkania ne
25	47	46.1	275	2	Q7XL00_ORYSA	Q7xl00 oryza sativ
26	47	46.1	528	2	Q7VWG6_BORPE	Q7vwg6 bordetella
27	47	46.1	528	2	Q7WL62_BORBR	Q7wl62 bordetella
28	47	46.1	530	2	Q7MPU6_VIBVY	Q7mpu6 vibrio vuln
29	47	46.1	841	2	Q7USV0_RHOBA	Q7usv0 rhodopirell
30	46	45.1	231	2	Q45543_BACSU	Q45543 bacillus su
31	46	45.1	326	2	Q9CJD6_LACLA	Q9cjd6 lactococcus
32	46	45.1	392	2	Q892L2_CLOTE	Q892l2 clostridium
33	46	45.1	437	2	Q62L19_BURMA	Q62l19 burkholderi
34	46	45.1	473	2	Q90D12_9HIV1	Q90d12 human immun
35	46	45.1	706	2	Q4P8Y5_USTMA	Q4p8y5 ustilago ma
36	46	45.1	746	2	Q8DQ40_STRR6	Q8dq40 streptococc
37	46	45.1	746	2	Q97R74_STRPN	Q97r74 streptococc
38	46	45.1	753	2	O85198_STRPN	O85198 streptococc
39	46	45.1	920	2	Q9JHY9_MESAU	Q9jhy9 mesocricetu
40	46	45.1	920	2	Q9JJK7_MESAU	Q9jjk7 mesocricetu
41	46	45.1	2584	2	Q9GSG2_CHEQU	Q9gsg2 cherax quad
42	45.5	44.6	189	2	Q6EGS1_POPTM	Q6egs1 populus tre
43	45.5	44.6	480	2	Q5V3W8_HALMA	Q5v3w8 haloarcula
44	45	44.1	106	1	Y1581_ARCFU	O28691 archaeoglob
45	45	44.1	162	2	Q881C5_PSESM	Q881c5 pseudomonas

ALIGNMENTS

RESULT 1
Q7Z7Q0_HUMAN
ID Q7Z7Q0_HUMAN PRELIMINARY; PRT; 825 AA.
AC Q7Z7Q0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APOB protein.
GN Name=APOB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Director MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC051278; AAH51278.1; -; mRNA.
DR GO; GO:0005319; F:lipid transporter activity; IEA.
DR GO; GO:0006869; P:lipid transport; IEA.
DR InterPro; IPR001747; Lipid_transprt_N.
DR Pfam; PF01347; Vitellogenin_N; 1.
DR SMART; SM00638; LPD_N; 1.
SQ SEQUENCE 825 AA; 92333 MW; 9004A128F9E6338E CRC64;

Query Match 100.0%; Score 102; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        685 IEIGLEGKGFEPTLEALFGK 704


RESULT 2
Q4ZG63_HUMAN
ID   Q4ZG63_HUMAN PRELIMINARY;      PRT;  3929 AA.
AC   Q4ZG63;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein APOB (Fragment).
GN   Name=APOB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Cotton M., Holmes A., Sander N.;
RT   "The sequence of Homo sapiens BAC clone RP11-83B6.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.H.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Waterston R.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RA   Wilson R.K.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC010872; AAX88848.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER    3929   3929
SQ   SEQUENCE   3929 AA;  441764 MW;  F05217A8149ED33F CRC64;

  Query Match             100.0%;  Score 102;  DB 2;  Length 3929;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 3
APOB_HUMAN
ID   APOB_HUMAN     STANDARD;      PRT;  4563 AA.
AC   P04114; O00502; P78479; P78480; P78481; Q13779; Q13785; Q13786;
AC   Q13787; Q13788; Q7Z600; Q9UMN0;
DT   01-NOV-1986 (Rel. 03, Created)
DT   01-NOV-1986 (Rel. 03, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Apolipoprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
DE   B-48 (Apo B-48)].
GN   Name=APOB;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87016385; PubMed=3763409;
RA   Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
RA   Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
RT   "Complete cDNA and derived protein sequence of human apolipoprotein B-
RT   100.";
RL   Nucleic Acids Res. 14:7501-7503(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS LYS-273; GLN-1218; LEU-2092;
RP   ALA-2365; LEU-2680; ILE-3732; PHE-3949; TYR-3964 AND GLU-4181.
RX   MEDLINE=88003974; PubMed=3652907;
RA   Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
RA   Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
RT   "DNA sequence of the human apolipoprotein B gene.";
RL   DNA 6:363-372(1987).
RN   [3]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS ILE-98; LYS-273; VAL-618; GLN-1218;
RP   LEU-2092; ALA-2365; LEU-2680; ILE-3732; PHE-3949; TYR-3964 AND
RP   GLU-4181.
RX   MEDLINE=87008488; PubMed=3759943;
RA   Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
RA   Gotto A.M. Jr., Chan L.;
RT   "The complete cDNA and amino acid sequence of human apolipoprotein B-
RT   100.";
RL   J. Biol. Chem. 261:12918-12921(1986).
RN   [4]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS LYS-273; GLN-1218; LEU-2092;
RP   ALA-2365; LEU-2680; ILE-3732 AND TYR-3964.
RX   MEDLINE=87041416; PubMed=3464946;
RA   Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
RA   Lee N., Brewer H.B. Jr.;
RT   "Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
RT   derived amino acid sequence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
RN   [5]
RP   NUCLEOTIDE SEQUENCE, AND VARIANTS LYS-273; VAL-618; GLN-1218;
RP   LEU-2092; ALA-2365 AND LEU-2680.
RX   MEDLINE=87161758; PubMed=3030729;
RA   Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
RA   Zannis V.I.;
RT   "The complete sequence and structural analysis of human apolipoprotein
RT   B-100: relationship between apoB-100 and apoB-48 forms.";
RL   EMBO J. 5:3495-3507(1986).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LYS-273; GLN-1218;
RP   LEU-2092; ALA-2365; LEU-2680; ASP-3319; THR-3427; GLN-3432; ILE-3732;
RP   PHE-3949; TYR-3964 AND GLU-4181.
RA   Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA   Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 1-1670, AND VARIANTS ILE-98; LYS-273 AND
RP   GLN-1218.
RX   MEDLINE=86287319; PubMed=3461454;
RA   Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.,
RA   Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
RT   "Analysis of cDNA clones encoding the entire B-26 region of human
RT   apolipoprotein B.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986).
RN   [8]
RP   NUCLEOTIDE SEQUENCE OF 1-291, AND VARIANT LYS-273.
RX   MEDLINE=86149325; PubMed=3513177;
RA   Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
RA   Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.;
RT   "Isolation of a cDNA clone encoding the amino-terminal region of human
RT   apolipoprotein B.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986).
RN   [9]
RP   PARTIAL PROTEIN SEQUENCE, DISULFIDE BONDS, AND VARIANT ILE-98.
RX   MEDLINE=90319144; PubMed=2115173;
RA   Yang C.Y., Kim T.W., Weng S.A., Lee B.R., Yang M.L., Gotto A.M. Jr.;
RT   "Isolation and characterization of sulfhydryl and disulfide peptides
RT   of human apolipoprotein B-100.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:5523-5527(1990).
RN   [10]
```

```
RP   NUCLEOTIDE SEQUENCE OF 485-1044.
RC   TISSUE=Liver;
RX   MEDLINE=86094221; PubMed=3001697;
RA   Law S.W., Lackner K.J., Hospattankar A.V., Anchors J.M.,
RA   Sakaguchi A.Y., Naylor S.L., Brewer H.B. Jr.;
RT   "Human apolipoprotein B-100: cloning, analysis of liver mRNA, and
RT   assignment of the gene to chromosome 2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:8340-8344(1985).
RN   [11]
RP   NUCLEOTIDE SEQUENCE OF 709-906.
RX   MEDLINE=85270450; PubMed=3860836;
RA   Deeb S.S., Motulsky A.G., Albers J.J.;
RT   "A partial cDNA clone for human apolipoprotein B.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
RN   [12]
RP   PROTEIN SEQUENCE OF 873-896 AND 3113-3137.
RX   MEDLINE=84208786; PubMed=6373369; DOI=10.1016/0014-5793(84)81378-2;
RA   LeBoeuf R.C., Miller C., Shively J.E., Schumaker V.N., Balla M.A.,
RA   Lusis A.J.;
RT   "Human apolipoprotein B: partial amino acid sequence.";
RL   FEBS Lett. 170:105-108(1984).
RN   [13]
RP   NUCLEOTIDE SEQUENCE OF 1042-1232, AND VARIANT GLN-1218.
RX   MEDLINE=89291895; PubMed=2567736;
RA   Huang L.S., Ripps M.E., Korman S.H., Deckelbaum R.J., Breslow J.L.;
RT   "Hypobetalipoproteinemia due to an apolipoprotein B gene exon 21
RT   deletion derived by Alu-Alu recombination.";
RL   J. Biol. Chem. 264:11394-11400(1989).
RN   [14]
RP   NUCLEOTIDE SEQUENCE OF 1282-4503, AND VARIANTS LEU-2092; ALA-2365;
RP   LEU-2680; PHE-3949; TYR-3964 AND GLU-4181.
RX   MEDLINE=87191999; PubMed=2883086; DOI=10.1016/0378-1119(86)90383-5;
RA   Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
RT   "Analysis of the human apolipoprotein B gene; complete structure of
RT   the B-74 region.";
RL   Gene 49:29-51(1986).
RN   [15]
RP   NUCLEOTIDE SEQUENCE OF 1671-2398, AND VARIANTS LEU-2092 AND ALA-2365.
RX   MEDLINE=88050832; PubMed=3676265;
RA   Hardman D.A., Protter A.A., Chen G.C., Schilling J.W., Sato K.Y.,
RA   Lau K., Yamanaka M., Mikita T., Miller J., Crisp T., McEnroe G.,
RA   Scarborough R.M., Kane J.P.;
RT   "Structural comparison of human apolipoproteins B-48 and B-100.";
RL   Biochemistry 26:5478-5486(1987).
RN   [16]
RP   NUCLEOTIDE SEQUENCE OF 1937-2018 AND 3811-4334, AND VARIANTS PHE-3949;
RP   TYR-3964 AND GLU-4181.
RX   MEDLINE=86093680; PubMed=3841204;
RA   Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
RA   Bjursell G.;
RT   "Molecular cloning of human apolipoprotein B cDNA.";
RL   Nucleic Acids Res. 13:8813-8826(1985).
RN   [17]
RP   NUCLEOTIDE SEQUENCE OF 2115-2179.
RC   TISSUE=Small intestine;
RX   MEDLINE=87301727; PubMed=3621347; DOI=10.1016/0092-8674(87)90510-1;
RA   Powell L.M., Wallis S.C., Pease R.J., Edwards Y.H., Knott T.J.,
RA   Scott J.;
RT   "A novel form of tissue-specific RNA processing produces
RT   apolipoprotein-B48 in intestine.";
RL   Cell 50:831-840(1987).
RN   [18]
RP   NUCLEOTIDE SEQUENCE OF 2127-2179.
RX   MEDLINE=88158075; PubMed=2450346;
RA   Higuchi K., Hospattankar A.V., Law S.W., Meglin N., Cortright J.,
RA   Brewer H.B. Jr.;
RT   "Human apolipoprotein B (apoB) mRNA: identification of two distinct
RT   apoB mRNAs, an mRNA with the apoB-100 sequence and an apoB mRNA
RT   containing a premature in-frame translational stop codon, in both
RT   liver and intestine.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1772-1776(1988).
RN   [19]
RP   NUCLEOTIDE SEQUENCE OF 2129-2235.
RX   PubMed=3426612;
RA   Hardman D.A., Protter A.A., Schilling J.W., Kane J.P.;
RT   "Carboxyl terminal analysis of human B-48 protein confirms the novel
RT   mechanism proposed for chain termination.";
RL   Biochem. Biophys. Res. Commun. 149:1214-1219(1987).
RN   [20]
RP   PROTEIN SEQUENCE OF 2169-2179.
RX   MEDLINE=88049670; PubMed=2445342;
RA   Hospattankar A.V., Higuchi K., Law S.W., Meglin N., Brewer H.B. Jr.;
RT   "Identification of a novel in-frame translational stop codon in human
RT   intestine apoB mRNA.";
RL   Biochem. Biophys. Res. Commun. 148:279-285(1987).
RN   [21]
RP   NUCLEOTIDE SEQUENCE OF 3056-3159.
RX   MEDLINE=86041888; PubMed=3903660;
RA   Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
RA   Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
RT   "Human apolipoprotein B: identification of cDNA clones and
RT   characterization of mRNA.";
RL   Nucleic Acids Res. 13:6937-6953(1985).
RN   [22]
RP   NUCLEOTIDE SEQUENCE OF 3109-4563.
RX   MEDLINE=85300528; PubMed=2994225;
RA   Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
RA   Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
RA   Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
RA   Mahley R.W., Scott J.;
RT   "Human apolipoprotein B: structure of carboxyl-terminal domains, sites
RT   of gene expression, and chromosomal localization.";
RL   Science 230:37-43(1985).
RN   [23]
RP   NUCLEOTIDE SEQUENCE OF 3728-4563, AND VARIANTS ILE-3732; PHE-3949;
RP   TYR-3964 AND GLU-4181.
RX   MEDLINE=86042646; PubMed=2932736;

  Query Match             100.0%;  Score 102;  DB 1;  Length 4563;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        688 IEIGLEGKGFEPTLEALFGK 707


RESULT 4
Q8CGG8_MOUSE
ID   Q8CGG8_MOUSE PRELIMINARY;      PRT;  1477 AA.
AC   Q8CGG8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Apob protein (Fragment).
GN   Name=Apob;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
```

```
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC038263; AAH38263.1; -; mRNA.
DR   Ensembl; ENSMUSG00000020609; Mus musculus.
DR   MGI; MGI:88052; Apob.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0005792; C:microsome; IDA.
DR   GO; GO:0030301; P:cholesterol transport; IMP.
DR   GO; GO:0006629; P:lipid metabolism; IDA.
DR   GO; GO:0006642; P:triacylglycerol mobilization; IMP.
DR   InterPro; IPR009454; DUF1081.
DR   InterPro; IPR001747; Lipid_transprt_N.
DR   Pfam; PF06448; DUF1081; 1.
DR   Pfam; PF01347; Vitellogenin_N; 1.
DR   SMART; SM00638; LPD_N; 1.
FT   NON_TER    1477   1477
SQ   SEQUENCE   1477 AA;  165115 MW;  E174DF7B2C755F26 CRC64;

  Query Match             96.1%;  Score 98;  DB 2;  Length 1477;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-06;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        689 EIGLEGKGFEPTLEALFGK 707


RESULT 5
Q7TMA5_RAT
ID   Q7TMA5_RAT  PRELIMINARY;      PRT;  4743 AA.
AC   Q7TMA5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Aa1064 (Ac1-060).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Xu C.S., Li W.Q., Li Y.C., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
RA   Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F., Han H.P.,
RA   Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Xu C.S., Li W.Q., Li Y.C., Zhao L.F., Ma H., Wang L., Wang S.F.,
RA   Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J., Yan H.M.,
RA   Chang C.F., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the cyclin family.
DR   EMBL; AY318958; AAP85369.1; -; mRNA.
DR   EMBL; AY321317; AAP86249.1; -; mRNA.
DR   Ensembl; ENSRNOG00000005542; Rattus norvegicus.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0005319; F:lipid transporter activity; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   GO; GO:0000074; P:regulation of cell cycle; IEA.
DR   InterPro; IPR006670; Cyclin.
DR   InterPro; IPR004367; Cyclin_Cterm.
DR   InterPro; IPR006671; Cyclin_N.
DR   InterPro; IPR009454; DUF1081.
DR   InterPro; IPR001747; Lipid_transprt_N.
DR   Pfam; PF02984; Cyclin_C; 1.
DR   Pfam; PF00134; Cyclin_N; 1.
DR   Pfam; PF06448; DUF1081; 1.
DR   Pfam; PF01347; Vitellogenin_N; 1.
DR   SMART; SM00385; CYCLIN; 1.
DR   SMART; SM00638; LPD_N; 1.
KW   Cyclin.
SQ   SEQUENCE   4743 AA;  536019 MW;  B01AD103F8EC5320 CRC64;

  Query Match             96.1%;  Score 98;  DB 2;  Length 4743;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFGK 20
              ||||||||||||||||||||
Db        677 EIGLEGKGFEPTLEALFGK 695


RESULT 6
Q9I8I1_DICLA
ID   Q9I8I1_DICLA PRELIMINARY;      PRT;  103 AA.
AC   Q9I8I1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Apolipoprotein B-100 (Fragment).
GN   Name=apoB-100;
OS   Dicentrarchus labrax (European sea bass).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Moronidae; Dicentrarchus.
OX   NCBI_TaxID=13489;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Colitti M., Morassutti C., Venturini E., Stefanon B.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF276500; AAF79210.1; -; mRNA.
KW   Lipoprotein.
FT   NON_TER       1      1
FT   NON_TER     103    103
SQ   SEQUENCE   103 AA;  11599 MW;  1F2DC082ED8F6D70 CRC64;

  Query Match             91.2%;  Score 93;  DB 2;  Length 103;
  Best Local Similarity   80.0%;  Pred. No. 1.4e-06;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              :|:|:||||||||:||||||
Db         38 MEVGMEGKGFEPTVEALFGK 57


RESULT 7
Q4S6S1_TETNG
ID   Q4S6S1_TETNG PRELIMINARY;      PRT;  2674 AA.
AC   Q4S6S1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 14 SCAF14723, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00023152001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
```

```
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014723; CAG03661.1; -; Genomic_DNA.
FT   NON_TER     2674    2674
SQ   SEQUENCE   2674 AA;  295027 MW;  AB541A7E7008B18E CRC64;

  Query Match             88.2%;  Score 90;  DB 2;  Length 2674;
  Best Local Similarity   84.2%;  Pred. No. 0.00012;
  Matches   16;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFG 19
              :|||:||||||||:|||||
Db        608 LEIGMEGKGFEPTVEALFG 626


RESULT 8
Q9TUI6_MONDO
ID   Q9TUI6_MONDO PRELIMINARY;      PRT;  1763 AA.
AC   Q9TUI6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Apolipoprotein B (Fragment).
OS   Monodelphis domestica (Short-tailed grey opossum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX   NCBI_TaxID=13616;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Fujino T., Navaratnam N., Jarmuz A., von Haeselaer A., Scott J.;
RT   "C to U editing of apolipoprotein B mRNA in marsupials :
RT   identification and characterisation of APOBEC-1 from the American
RT   opossum Monodelphaus domestica.";
RL   Nucleic Acids Res. 0:0-0(1999).
DR   EMBL; AB027413; BAA86052.1; -; mRNA.
DR   GO; GO:0005319; F:lipid transporter activity; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   InterPro; IPR009454; DUF1081.
DR   InterPro; IPR001747; Lipid_transprt_N.
DR   Pfam; PF06448; DUF1081; 1.
DR   Pfam; PF01347; Vitellogenin_N; 1.
KW   Lipoprotein.
FT   NON_TER       1       1
SQ   SEQUENCE   1763 AA;  192329 MW;  DBEF8F87ED2D6289 CRC64;

  Query Match             72.5%;  Score 74;  DB 2;  Length 1763;
  Best Local Similarity   65.0%;  Pred. No. 0.027;
  Matches   13;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              :|:||| :|:|  |||||||
Db        279 VEVGLEAQGYEAALEALFGK 298


RESULT 9
Q5TZ29_BRARE
ID   Q5TZ29_BRARE PRELIMINARY;      PRT;  3730 AA.
AC   Q5TZ29;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Novel protein similar to vertebrate apolipoprotein B (Including Ag(X)
DE   antigen) (APOB).
GN   Name=OTTDARP00000005429; ORFNames=CH211-219I10.1-001;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hunter G.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX511210; CAH68927.1; -; Genomic_DNA.
DR   GO; GO:0005319; F:lipid transporter activity; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   InterPro; IPR009454; DUF1081.
DR   InterPro; IPR001747; Lipid_transprt_N.
DR   Pfam; PF06448; DUF1081; 1.
DR   Pfam; PF01347; Vitellogenin_N; 1.
DR   SMART; SM00638; LPD_N; 1.
KW   Lipoprotein.
SQ   SEQUENCE   3730 AA;  412588 MW;  DBC60A6CBFCEB69E CRC64;

  Query Match             68.6%;  Score 70;  DB 2;  Length 3730;
  Best Local Similarity   72.2%;  Pred. No. 0.24;
  Matches   13;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFG 19
              |||| ||| |||::|| |
Db        647 EIGLNGKGLEPTVDALIG 664


RESULT 10
Q57EG8_BRUAB
ID   Q57EG8_BRUAB PRELIMINARY;      PRT;   199 AA.
AC   Q57EG8;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Fe-Mn superoxide dismutase.
GN   OrderedLocusNames=BruAb1_0588;
OS   Brucella abortus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=235;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=9-941 / Biovar 1;
RX   PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA   Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,
RA   Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT   "Completion of the genome sequence of Brucella abortus and comparison
RT   to the highly similar genomes of Brucella melitensis and Brucella
RT   suis.";
RL   J. Bacteriol. 187:2715-2726(2005).
CC   -!- FUNCTION: Destroys radicals which are normally produced within the
CC       cells and which are toxic to biological systems (By similarity).
CC   -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC   -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC       family.
DR   EMBL; AE017223; AAX73966.1; -; Genomic_DNA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0004784; F:superoxide dismutase activity; IEA.
```

```
DR   GO; GO:0006801; P:superoxide metabolism; IEA.
KW   Complete proteome; Oxidoreductase.
SQ   SEQUENCE   199 AA;  22540 MW;  8C5D1A240858D546 CRC64;

  Query Match             50.0%;  Score 51;  DB 2;  Length 199;
  Best Local Similarity   58.8%;  Pred. No. 13;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GLEGKGFEPTLEALFGK 20
              ||||| ||  ::  |||
Db         47 GLEGKSFEEIVKESFGK 63


RESULT 11
Q762M9_9EUCA
ID   Q762M9_9EUCA PRELIMINARY;      PRT;  2534 AA.
AC   Q762M9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Vitellogenin precursor.
GN   Name=Vg;
OS   Pandalus hypsinotus.
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
OC   Pandalidae; Pandalus.
OX   NCBI_TaxID=242778;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tsutsui N., Saido-Sakanaka H., Yang W.J., Jayasankar V., Jasmani S.,
RA   Okuno A., Ohira T., Okumura T., Aida K., Wilder M.N.;
RT   "Molecular characterization of a cDNA encoding vitellogenin in the
RT   coonstriped shrimp, Pandalus hypsinotus and site of vitellogenin mRNA
RT   expression.";
RL   J. Exp. Zool., A, Comp. Exp. Biol. 301A:802-814(2004).
DR   EMBL; AB117524; BAD11098.1; -; mRNA.
DR   GO; GO:0005319; F:lipid transporter activity; IEA.
DR   GO; GO:0006869; P:lipid transport; IEA.
DR   InterPro; IPR009454; DUF1081.
DR   InterPro; IPR001747; Lipid_transprt_N.
DR   InterPro; IPR001846; VWF_D.
DR   Pfam; PF06448; DUF1081; 1.
DR   Pfam; PF01347; Vitellogenin_N; 1.
DR   Pfam; PF00094; VWD; 1.
DR   SMART; SM00638; LPD_N; 1.
DR   SMART; SM00216; VWD; 1.
KW   Signal.
FT   SIGNAL        1     18       Potential.
SQ   SEQUENCE   2534 AA;  283596 MW;  AEFC2E56E5F5E0AB CRC64;

  Query Match             50.0%;  Score 51;  DB 2;  Length 2534;
  Best Local Similarity   61.1%;  Pred. No. 1.7e+02;
  Matches   11;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 EIGLEGKGFEPTLEALFG 19
              |||   :| || || |||
Db        675 EIGARIEGLEPILEDLFG 692


RESULT 12
Q97JD2_CLOAB
ID   Q97JD2_CLOAB PRELIMINARY;      PRT;   159 AA.
AC   Q97JD2;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Phosphotransferase system IIA component.
GN   OrderedLocusNames=CAC1354;
OS   Clostridium acetobutylicum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1488;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX   MEDLINE=21359325; PubMed=11466286;
RX   DOI=10.1128/JB.183.16.4823-4838.2001;
RA   Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA   Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA   Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
RA   Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
RT   "Genome sequence and comparative analysis of the solvent-producing
RT   bacterium Clostridium acetobutylicum.";
RL   J. Bacteriol. 183:4823-4838(2001).
DR   EMBL; AE007647; AAK79322.1; -; Genomic_DNA.
DR   PIR; G97066; G97066.
DR   HSSP; P08837; 1GLC.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005351; F:sugar porter activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR001127; PTS_EIIA.
DR   Pfam; PF00358; PTS_EIIA_1; 1.
DR   ProDom; PD002243; PTS_EIIA; 1.
DR   TIGRFAMs; TIGR00830; PTBA; 1.
DR   PROSITE; PS00371; PTS_EIIA_1; 1.
KW   Complete proteome; Transferase.
SQ   SEQUENCE   159 AA;  17273 MW;  0A2882A6BE1DD7A4 CRC64;

  Query Match             49.0%;  Score 50;  DB 2;  Length 159;
  Best Local Similarity   69.2%;  Pred. No. 14;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 IGLEGKGFEPTLE 15
              : |||||||| :|
Db         85 VKLEGKGFEPLVE 97


RESULT 13
Y3508_XANAC
ID   Y3508_XANAC    STANDARD;      PRT;   314 AA.
AC   Q8PGV3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Hypothetical UPF0230 protein XAC3508.
GN   OrderedLocusNames=XAC3508;
OS   Xanthomonas axonopodis (pv. citri).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xanthomonas.
OX   NCBI_TaxID=92829;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=306 / ATCC 13902 / XV 101;
RX   MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA   da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA   Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA   Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA   Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
RA   Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA   El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA   Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA   Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA   Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA   Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA   Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA   Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA   Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA   Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA   Setubal J.C., Kitajima J.P.;
RT   "Comparison of the genomes of two Xanthomonas pathogens with differing
RT   host specificities.";
RL   Nature 417:459-463(2002).
CC   -!- SIMILARITY: Belongs to the UPF0230 (degV) family.
CC   ---------------------------------------------------------------------
```

```
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AE011999; AAM38352.1; -; Genomic_DNA.
DR   InterPro; IPR003797; DegV.
DR   Pfam; PF02645; DegV; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   314 AA;  34199 MW;  E8FB8F5E2C3DB25E CRC64;

  Query Match             48.0%;  Score 49;  DB 1;  Length 314;
  Best Local Similarity   75.0%;  Pred. No. 41;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 KGFEPTLEALFG 19
              |||||: | |||
Db        226 KGFEPSAEKLFG 237


RESULT 14
Q9LLC2_ASPOF
ID   Q9LLC2_ASPOF PRELIMINARY;      PRT;   284 AA.
AC   Q9LLC2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Xyloglucan endotransglycosylase XET2 (EC 2.4.1.207).
GN   Name=AoXET2;
OS   Asparagus officinalis (Garden asparagus).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
OC   Asparagus.
OX   NCBI_TaxID=4686;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   O'Donoghue E.M., Somerfield S.D., Sinclair B.K., Coupe S.A.;
RT   "Xyloglucan endotransglycosylase: a role after growth cessation in
RT   harvested asparagus.";
RL   Aust. J. Plant Physiol. 28:349-361(2001).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC       in beta-D-glucans containing 1,3- and 1,4-bonds.
DR   EMBL; AF223420; AAF80591.1; -; mRNA.
DR   HSSP; P23904; 1AJK.
DR   GO; GO:0048046; C:apoplast; IEA.
DR   GO; GO:0005618; C:cell wall; IEA.
DR   GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR   GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
DR   GO; GO:0016762; F:xyloglucan:xyloglucosyl transferase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0006073; P:glucan metabolism; IEA.
DR   InterPro; IPR008264; Beta_glucanase.
DR   InterPro; IPR008263; Glyco_hyd16_AS.
DR   InterPro; IPR000757; Glyco_hydro_16.
DR   InterPro; IPR010713; XET_C.
DR   Pfam; PF00722; Glyco_hydro_16; 1.
DR   Pfam; PF06955; XET_C; 1.
DR   PRINTS; PR00737; GLHYDRLASE16.
DR   PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
KW   Glycosidase; Glycosyltransferase; Hydrolase; Transferase.
SQ   SEQUENCE   284 AA;  31706 MW;  9DF014C513515E18 CRC64;

  Query Match             47.1%;  Score 48;  DB 2;  Length 284;
  Best Local Similarity   71.4%;  Pred. No. 54;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 GKGFEPTLEALFGK 20
              | ||| | | ||||
Db         53 GSGFESTHEYLFGK 66


RESULT 15
Q6AB55_PROAC
ID   Q6AB55_PROAC PRELIMINARY;      PRT;   449 AA.
AC   Q6AB55;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative flavin-containing amine oxidase (EC 1.4.3.-).
GN   OrderedLocusNames=PPA0250;
OS   Propionibacterium acnes.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Propionibacterineae; Propionibacteriaceae; Propionibacterium.
OX   NCBI_TaxID=1747;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KPA171202 / DSM 16379;
RX   PubMed=15286373; DOI=10.1126/science.1100330;
RA   Brueggemann H., Henne A., Hoster F., Liesegang H., Wiezer A.,
RA   Strittmatter A., Hujer S., Duerre P., Gottschalk G.;
RT   "The complete genome sequence of Propionibacterium acnes, a commensal
RT   of human skin.";
RL   Science 305:671-673(2004).
DR   EMBL; AE017283; AAT82011.1; -; Genomic_DNA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001613; Amineoxid_fl.
DR   InterPro; IPR002937; Amino_oxidase.
DR   InterPro; IPR000205; NAD_BS.
DR   Pfam; PF01593; Amino_oxidase; 1.
DR   PRINTS; PR00757; AMINEOXDASEF.
KW   Complete proteome; Oxidoreductase.
SQ   SEQUENCE   449 AA;  47713 MW;  F3EFEF2F1E2733FC CRC64;

  Query Match             47.1%;  Score 48;  DB 2;  Length 449;
  Best Local Similarity   40.0%;  Pred. No. 86;
  Matches    8;  Conservative    5;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 IEIGLEGKGFEPTLEALFGK 20
              : :||  : ||  :|: |||
Db        351 LSVGLRQRAFEEVVESAFGK 370


Search completed: March 21, 2006, 18:56:10
Job time : 238 secs
```

This Page Blank (uspto)